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                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCCGTCGTCAACGAGGGACCCGCTGCAGCTCTCCTTCGGCCTCACGCTCATGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCATCGACGTGGACGAGAACCAGCTTTTAATAACAAACATCTGGCTAAAACTAGAGT
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           Length 3126;
                                                                          3;
                                                                          Indels
           DB 11;
   Score 281.6; DB 11;
Pred. No. 7e-44;
0; Mismatches 469;
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       18.9%;
55.0%;
Query Match 18.9
Best Local Similarity 55.0
Matches 576; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enriched mouse cDNA library
                                                                                                                                                                                                                        on functional annotation
                                                                                                                                                 Exploration Research
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                                     Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                 Consortium and the RIKEN Genome
                                                                                                                                                                                   Group Phase I & II Team.
Analysis of the mouse transcriptome based
of 60,770 full-length cDNAs
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/db_xref="MGI:2407635"
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/clone="A73007P14"
/clone_type="cerebellum"
/clone_lib="RIKEN full-length of dev_stage="7 days neonate"
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                                                                                                                                                                                                                                                                                       Nature 420, 563-573 (2002)
6 (bases 1 to 3126)
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/codon start=1
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LDITYHFWWRLPLPIYFIVWIIPCLLRSFLTSLVFYLPTGSGERWTLSISVLLSTTVP
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KSAIEGVKYIAETMKSDQESNNAAEBWKYVAMVMDHILLGVFMLVCLIGTLAVFAGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                    Research Group in Riken
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                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="unnamed protein product; cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (MGD|MGI:87885, GB|NM_007389, evidence: BLASTN, 99%, match=1763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 GCGCCGCTCGCACTTGGCGGCCCCGCGGGCCTGCTGCTGCTGCTGTGCCTGTTCTGCTCTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 ACAGCTGATCCAGCTTATCAATGTGGATGAAGTAAATCAGATTGTGACAACCAATGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 GCTAAAACTAGAGTGGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 TCTGAAACAGCAATGGGTCGATTACAACTTGAAATGGAATCCAGATGACTATGGAGGAGT
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Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.8%; Score 280.4; DB 11; Length 4290; 54.5%; Pred. No. 1.3e-43; ive 0; Mismatches 465; Indels 0;
                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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/db_xref="MG1:5391229"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="0 day neonate"
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                                                                                                                                                                                                        AKU29177
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched alpha polypeptide 1 (muscle), full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonake, S., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNs.
Nature 420, 563-573 (2002)
6 (bases 1 to 4290)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
            Mus musculus (house mouse)
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                                                                                                                                                                                                    West Gude Drive,
Lu, F., Murphy, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 29; Length 1374;
                                                                                                                                                                                     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude D. Rockville, MD 20850, USA. This sequence was made by sequencing genomic exons and them based on alignment.
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F. Ferritard,S., Wang,G., Zheng,X.H., White,T.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 278.4; DB 29;
Pred. No. 2.2e-43;
0; Mismatches 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .1374
/organism="Mus musculus"
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/db_xref="taxon:10090"
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/gene="CHRNA1"
/locus_tag="HCM2488"
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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56.2%;
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242 332 302 452 422 512 572 542 632 599 689 629 749 719 809 779

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123 AGTGGAAGACCACGCCAGGTCGTGGAGCTCACGTGGGCCTGCAGCTGATACAGCTCAT 182	453 GGGCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTT 423 AGCCATCTTTAAAAGCTACTGAGATCATCGTCACCCACTTTCCCTTTT 513 AGCCATCTTTAAAAGCTACTGAGATCATCGTCACCCACTTTCCCTTTT 613 AGCCATCATGAAGCTGAGCACCTGAGCCTACGACGCTTTTCCTTTGTCACGAATGCTACGTGGAGC 633 AGCCCAGCACGAGCACCTGAGCACTTTTTTCACGAGTGGTGGAGC 634 AGCCACCAGACCTGAGCACCTACGAGAGCACCTGAGGCGAATGCTGTGTGTG	RESULT 10 CD013891 LOCUS DD79066 Single gene library Homo sapiens CDNA, mRNA sequence. DD7013891 LOCUS DD7013891 LOCUS DD7013891 CD013891
0 0 0 0 0 0 0 0 0 0	RESULT 9 AY406230 IOCUGS IOCUGS IOCUGS ACCESSION PAY66230 AY406230 ACCESSION AY406230 AY406230 AY406230 AY406230 AY406230 AY406230 AY406230 AY406230 IG 3:39762204 KEYWORDS GSS. SOURCE GSS. SOURCE Homo sapiens (human) BURATYOTA: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; (hases 1 to 134) REFERENCE IOCHAMMALIA: Tanenbaum, D.M.: (Arello, D.R.: Lu, F., Murphy, B.; FATTICE AUTHORS INCATIGN AUTHORS JOURNAL SCIENCE 302 (5652), 1960-1963 (2003) REFERENCE JOURNAL SCIENCE (Janowskit, S., Nielson, R.; Thomas, P.; Kejariwal, A.; TITLE INCATIGN AUTHORS JOURNAL SCIENCE 302 (5652), 1960-1963 (2003) REFERENCE AUTHORS LOAD, M. Tanenbaum, D.M.: (Arello, D.R.: Lu, F.; Murphy, B.; FETTICE (Janowskit, S., Nielson, R.; Thomas, P.; Kejariwal, A.; TITLE AUTHORS JOURNAL AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS TITLE Direct Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA COMMENT ROCKVILLE, MD 20850, USA AUTHORS THIS SEQUENCE AUTHORS THIS SEQUENCE AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS THIS SEQUENCE AUTHORS THIS SEQUENCE AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHORS THIS SEQUENCE AUTHORS AUTHO	ORIGIN ORETY Match Query Match Best Local Similarity 56.0%; Pred. No. 9e-43; Matches 564; Conservative 0; Mismatches 438; Indels 6; Gaps 2; Qy 33 GGGCCGGGGCCTGCTGCTGCTGCTGCTGCTGCTGGCGGGGCAGCGCTGGG 92

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CGAAGGGTTCGACAGCACGTATCCAACGAACGTGGTGCTGCGGAACAACGGCTCGTGTCT 440
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                         1 (bases 1 to 1436)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wangy,G., Androws,M.D. and Cargill,M.
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                   Clark, A.G., Clanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission

Direct Submission

Submitteed (16-N0V-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Pred. No. 1.1e-41;
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/db_xref="taxon:10090'
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                                                           GACGAGAAGAACCAGCTTTTAATAACAAACATCTGGCTAAAAACTAGAGTGGAATGATATG 279
                                                                                                                                          AACTIGAGGIGGAACACTICAGAITICGGCGGGGICAAAGAITIAAGAGIGCCACCCCAC 339
                                                                                                                                                                               201 AAGCTGAAGTGGAACCCCTCTGACTATGGTGGGGCAGAGTTCATGCGTGTCCCTGCACAG 260
                                                                                                                                                                                                                      AGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACAGCACG 399
                                                                                                                                                                                                                                                         261 AAGATCTGGAAGCCAGACATTGTGCTGTATAACAATGCTGTTGGGGATTTCCAGGTGGAC 320
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Mus musculus CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,
580 GGGGGCGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAATAGGAGTCCCC
                                                                                                GATGAAGTAAACCAGATCATGGAGACCAACCTGTGGCTCAAGCAAATCTGGAATGACTAC
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AY402874 11-DEC-2003 1436 bp DNA linear GSS 15-DEC-2003 Pan troglodytes CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,
/note="Organ: head; Vector: pOT2; Site 1: BcoR1; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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                                                                                                                                                                                                                                21 CTCGCACTTGGCGCCCCGCCGGGCCTGCTGCTGCTGCTGTGCCTGCTCTGGCCTGGCCGAGGGG
                                                                                                                                                                                                                                                                           81 GGCACGCTGCGGGTACCACGAGAAGCGGCTACTGCACCTATTGGACCACTACAACGT
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
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1 (bases 1 to 1436)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Pred. No. 8.8e-42;
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Pan troglodytes
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GH15518.5prime GH Drosophila melanogaster head port Drosophila melanogaster read port Drosophila melanogaster read port Drosophila melanogaster consequence GH15518 5 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30Dl-30El;: 04/10/2001, mRNA sequence. AI29281
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea; Drosophilidae, Drosophila.
1 (Dases 1 to 607)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
                741 TCTGATCGTGCCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCC
                                                                                                                                                                                                                         719 cGACTGTGGGGAGAAGGTGACGCTCTGCATCTCCGTGCTCCTCTCCTGACGGTCTTTCT
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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE00326: arm:2L [9617316,9882551]
estimated-cyto:30C7-30F4: 04/10/2001
Plate: GH.155 row: B column: 6
High quality sequence stop: 521
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/lab_host="DHS - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Drosophila melanogaster
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/db_xref="taxon:7227"
/clone="GH15518"
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857 999

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AK080475

2010 bp mRNA linear HTC 19-SEP-2003 Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730038F14 product:NBURONAL NICOTINIC AKCEYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.

AK080475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishiner, T., Harada, M., Pujiwake, R., Matsumoto, R., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer General General Connerges. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                   .000 GACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTGCCGTGGGTG 1059
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Nature 420, 563-573 (2002)
6 (bases 1 to 2010)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
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Mus musculus (house mouse)
Mus musculus
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rodd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Pred. No. 1.8e-40;
0; Mismatches 445;

    1436
    /organism="Pan troglodytes"
/mol_type="genomic DNA"
    /db_xref="taxon:9598"

                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CHRNA3"
/locus_tag="HCM1369"
                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, I., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsto, N., Santo, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibara, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Direct Submission
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/clone_lib="RIKEN full-length enriched mouse cDNA library'
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Please visit our web site for further details.
Please visit our web site for further details.
URL:http://fentom.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

7, 2004, 11:09:28 ; Search time 42.6667 Seconds (without alignments) 3284.615 Million cell updates/sec May on: Run

US-09-303-232-4 2665 Perfect score:

1 MGGRARRSHLAAPAGLILLL......LFTIIATLAVLLSAPHIMVS 496 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Description	Aav50815 H. viresc	2	, E	Dro			Aaw44153 Human neu	Aaw09025 Neuronal	. ,	Aab82690 Nicotinic	-	Abq70492 Human neu	Human		Human	Human	Aaw69216 V274T var	Aab50015 Mutant hu	_	Ade57308 Rat Prote	Rat	Muta			_
	ID	AAY50815	AAY50814	AAY50816	ABB63683	AAW12368	ABB60432	AAW44153	AAW09025	AAB24088	AAB82690	AAB50012	ABG70492	ABB82435	ADA10874	ADD47051	ADE57310	AAW69216	AAB50015	AAB 50016	ADE57308	ADD47049	AAB50017	AAW12369	AAE12824	ABP96318
	DB		m	m	4	7	4	7	7	М	4	4	2	S	7	7	7	7	4	4	7	7	4	~	4	9
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	Score	2665	1.850	1803.5	1417.5	1267	1253	1246	1246	1246	1246	1246	1246	1246	1246	1246	1246	1242	1240	1236		1232.5	1230	1219.5	1053.5	1053.5
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Aab50014 Chimeric Aab50018 Mature ce	Abb60716 Drosophil Aao17243 Modified		Ade57318 Human Pro Aaw09022 Neuronal	Adal0857 Human neu	Aaw44155 Human neu		Aaw09021 Neuronal	Abg61850 Prostate	Abq31800 Human neu		Ada10855 Human neu	Adc71171 Human 205	Adc71169 Human 205		Human	Human
AAB50014 AAB50018	ABB60716 AAO17243	ADE57314	ADE57318 AAW09022	ADA10857	AAW44155	AAR73966	AAW09021	ABG61850	ABG31800	ABB82430	ADA10855	ADC71171	ADC71169	ADD45584	ADE59169	ADA83810
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226	2 7 2 6 6 6	30	32 32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Acetyl-choline receptor, nicotinic, insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR. H. virescens acetyl-choline receptor protein from clone Hva7-1. AAY50815 standard; protein; 496 AA. 17-FEB-2000 (first entry) AAY50815; AAY50815 ID AAY5 RESULT 1

98DE-01019829 98DE-01019829 Heliothis virescens DE19819829-A1 04-MAY-1998; 04-MAY-1998; 11-NOV-1999

(FARB) BAYER AG.

Adamczewski M, Oellers N,

Schulte T;

WPI; 2000-014207/02. N-PSDB; AAZ24476.

New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Example 1a; Page 17-19; 26pp; German

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotranamission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens

Sequence 496 AA;

7:

Gaps

16;

Length 770;

136

354

16

196

474

414

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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere which neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved information of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                           295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 LLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                      NOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DLELRERSSKSLLANVLDIDDDFRH-----PQAQQPQCCRYYR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615 DISSERKHQILSÖVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LAAHSCF--GVDYELSLILKEIRVITDQMRKDDEDADISRDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetyl-choline receptor protein from clone Hva7-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 KFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMVS 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                          69.4%; Score 1850; DB 3; 70.0%; Pred. No. 2.4e-175;
                                                                                                                                                                                                                                                                                                        30; Mismatches
                              Example la; Page 12-14; 26pp; German
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Matches 361;
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                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                          TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA 300
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                                                                                                                                         LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120
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                                                                                                                                                                                                                                                                             YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEFYIDITFAVVIRRK
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                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid encoding a nicotinic acetylcholine receptor from
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                 Length 496;
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                5; DB 3;
4.5e-257;
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                 Score 2665;
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           Query Match
Best Local Similarity 100.
Marches 496; Conservative
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neurotransmission; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                             This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1) encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (1) are also used to recombinant production of (11). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPPARV- 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRL 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGGGDISSFVINGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APAGLILLICLIMPRGARCGYHEKRLLHHILDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPPPDLELRERSSKSLLANVLDIDDDFRH----PQAQQ-----PQCCRY---YRGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRMRELELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGPGCSIFRTDFRRSFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                  New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1803.5; DB 3; Pred. No. 5.8e-171; 53; Mismatches 78;
                                                                                                                                     Schulte T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                67.78;
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Best Local Similarity 68.73
Matches 347; Conservative
                                                                                                                                                             2000-014207/02.
                                                                                                                                                            WPI; 2000-014207/
N-PSDB; AAZ24477.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 501 AA;
                                                                                                                                    Adamczewski M,
                                                                                                         (FARB ) BAYER
        DE19819829-A1
                                                          04-MAY-1998;
                                11-NOV-1999
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
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                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%; Score 1417.5; DB 4; Length 311; 87.2%; Pred. No. 1.1e-132; ive 14; Mismatches 16; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 17841.
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CLFVFTLFTIIATVAVLLSAPHIIV 500
                                                                                                                                                       protein; 311
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                       standard;
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es 265; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
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E----DKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLDGVHCTPTTDS
                                                                                                                                                                                                                                                                                                                                                                                                                               GVICGRMTCSPTEEBILLHSGHPSEG-DPDLAKILEEVRYIANRFRDQDEEBAICNEWKF
                                                      LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                          YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                              TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                   VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG
                                                                                                                                                                                                                                                                                                                                                                                                           405 PQCCRYYRGG--EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 8088; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                     361 SATTPPPARVPPPDLELRERSSKSLLANVLD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The alphal subunit (AAW1236B) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarotoxin binding protein (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be used to produce subunit peptides for use as immunogens for preparing antibodies to permit affinity purification of subtypes and their histological location
                         61 LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120
       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated neuronal alpha-bungaro-toxin-binding protein DNA - used screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                         Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 502;
                                                                                                                                                                                                                                                                                                      Neuronal alpha-bungarotoxin binding protein alphal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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48.6%; Pred. No. 2.5e-117;
iive 83; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23. .502
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                   standard; protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 2A-B; 18pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-00413947
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                                                                                                                                                                                                                                                                                                                                                           ligand binding; ion channel.
                                                                                                                                                                                                                                                                     (first entry)
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nes 249; Conservative
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                                                                          PLLG 305
                                                                                                           PLLG 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lindstrom JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1989;
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                                                                                                                                                                                                                                                                     17-JUN-1997
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       242
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                                                                                                                                                                                                                             LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA 126
                                                                                                                                                                                                                                                                                DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                               -----ILFFQFN----CAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TILLSLTVFLNMVAETMP-----ATSDAVPLLGTYFNCIM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----RNEIYYNCCPEPYIDI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMVASSVVSTILILLNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP- 371
                                                                                                                                                                         8 SHLAAPPAGLILILICLIMPRGARC-GYHEKRLLHHILDHYNVLERPVVNESDPLQLSFGLT 66
                                                                                                                                                                                       insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                      232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALIGFTLPPDSGEKLSLGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAA------
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit; brain tissue; screening; NAChR; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEHHTAIGCNHKDIHLILKELQFITARMRKADDEAELIGDWKFAAMVVDR 498
                                                                                                                                                  102;
                                                                                                                    47.0%; Score 1253; DB 4; Length 498; 50.4%; Pred. No. 6.1e-116;
                                                                                                                                               53; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                     DLQLQDEGGGDISSFVTNGEWELIGV-PGK-----
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262. 284
/label= TMD2
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/label= signal
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/label= TMD1
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                                                                                                                                                Conservative
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                                                                                                                                 al Similarity
267; Conserv
                                                                                             Sequence 498 AA;
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The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or atteagonists provides information with respect to the identification and decign of compounds that are should lead to the identification and decign of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                               also
y of
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human neuronal nicotinic acetylcholine receptor subunits and DNA - al
transformed cells useful for screening cpds. Which modulate activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.8%; Score 1246; DB 2;
46.0%; Pred. No. 3.1e-115;
iive 86; Mismatches 126;
             290. 317
/label= TMD3
/note= "transmembrane domain"
'note= "transmembrane domain"
                                                                                                                                                            /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                           (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                              /label= cytoplasmic_loop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 80-81; 99pp; English
                                                                                                              note= "encoded
                                                                                                                                                                                                                                                                                                                                                             Harpold
                                                                                                                                                                                                                                                                                            93US-00028031.
                                                                                                                              462. .487
/label= TMD4
                                                                                                                                                                                                                                                              94WO-US002447
                                                             .461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.09
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                            Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-303024/37.
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV12197
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                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the receptor.
                                                                                                                                                                                                                                                            08-MAR-1994;
                                                                                                                                                                                                                                                                                            08-MAR-1993;
                                                                                                                                                                                                                             15-SEP-1994
                                                                                                                                                                                                                                                                                                                                                            Elliott KJ,
                 Domain
                                                                Domain
                                                                                                                              Domain
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71 63 123 191

DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131

72 64 132

DVDEKNOVLTINIWLOMSWIDHYLOWNVSEYPGVKTVRFPDGGIWKPDILLYNSADERFD

12 APAGLILLICLIWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLOLSFGLTLMQII

ð 엄 à qq à qq ð g à g

251

124 ATFHINVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQ 183

STYPTHVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ

CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311

184 252

192

DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP

us-09-303-232-4.rag

9

360 360

251

452 452

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STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
                                                                                                                                                                                                                               Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; oytostatic; notoropic; neuroprotective, antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neurooral disorder; glial disorder; astrocytal disorder; glial disorder; astrocytal disorder; anglogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; blastocoelic disorder;
                                               ------DPDLAKILEEVRYIANRFRCQDE
                                                                                                             DEGGGDISSFVTNGEWELLGVPGKRNELYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                     CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
                                                                                                                                                                                                                                                                                                                                                                                        --VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                361 ORRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO2145 protein sequence SEQ ID NO:77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory disorder; immunologic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                     --SATTPPPAR---
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99WO-US012252.
99US-0141037P.
99US-0143048P.
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99WO-US030911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
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N-PSDB; AAC58395.
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Watanabe CK,
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02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAV48239). Host cells, esp. mammalian cells or amphibian occytes, expressing the recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24), AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity
360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding nicotinic acetyl:choline receptor sub-units - used in screening to determine the effect of drugs on the receptor.
                                          MIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                            SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
                                                                                          --VPPPPDLELRERSSKSLLANVLD
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                                                                                                                                     ORRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                  393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
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MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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                                                                                                                                                                                                                                                                          DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                    SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSADNFV 494
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46.0%; Pred. No. 3.1e-115;
iive 86; Mismatches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW09025 standard; protein; 502 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US009775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ligand-gated receptor
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ROY MA;

Hillan KJ,

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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355, PRO619, PRO1030, PRO809, PRO310, PRO1030, PRO1030, PRO1030, PRO1030, PRO1030, PRO1030, PRO1030, PRO1031, PRO1181, PRO1182, PRO1184, PRO1187, PRO1281, PRO181, PRO1181, PRO1182, PRO1187, PRO1281, PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds more to treat various conditions, including those characterised by coverapression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, and various head and neck tumours), lateramias and immunia malfarent control or the present of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC5836 represent PCR primers and Pybridisastion probes used in the isolation of the human PRO sequences. AAC58365 to AAC58366 and AAB4057 to AAB24089 represent human PRO polynucleotide and protein sequences given in the exemplification of the
                                          Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer.
                                                                                                                                                                                    English.
                                                                                                                                                                               286pp;
                                                                                                                                                                               Claim 61; Fig 58;
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Gaps 70; Length 502; 46.8%; Score 1246; DB 3; Length 5 46.0%; Pred. No. 3.1e-115; ive 86; Mismatches 126; Indels 240; Conservative Similarity Sequence 502 AA; Query Match Local Matches

9 360 301 MINGLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHK 360 DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300 -VPPPPDLELRERSSKSLLANVLD 392 393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE 452 DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131 STYPINVVVRNNGSCLYVPPGLFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191 CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311 12 APAGLLILLCLIMPRGARCGYHEKRILHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71 SPGGVWLALAASLIHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM 63 361 ORRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG--------SATTPPPAR---72 124 132 192 184 312 252 361 a 셤 g à 원 δ qq $\stackrel{>}{\circ}$ à g õ q à δ g ò

Disclosure; Page 252-254; 260pp; English.

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acetylcholine binding procein, AChBP, mollusc; ligand-binding protein; ligand-gated ion channel; crystal; drug design; protein co-ordinate data; schizophrenia; Alzheimer's disease; nicotine addiction; Tourette's syndrome; therapy; nootropic; neuroprotective.
                                                                                                                                                                                               108. .115
/note= "conserved ligand-binding region, residues Trp108
and Tyril5 are essential"
                                                                                                                                                                                                                                                                           residues Tyr210,
                                                                                                                                                                                                                                       /note= "conserved ligand-binding region, residues Trp171 and Tyr173 are essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or
                                                                                                                                                                                                                                                                         /note= "conserved ligand-binding region, Cys212, Cys213 and Tyr217 are essential"
                                                                                                Nicotinic acetylcholine receptor; nAChR; human;
                                                                           Nicotinic acetylcholine receptor alpha7.
                                                                                                                                                                                                                                                                                                                                                                                                         (TEWE-) STICHTING TECH WETENSCHAPPEN.
                                                                                                                                                                                      Location/Qualifiers
         AAB82690 standard; protein; 502
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31-OCT-2000; 2000EP-00203810.
                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            schizophrenia.
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                                AAB82690;
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                                                                                                                                                                                                 Region
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                                                                                                                                                                 Homo
AAB82690
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The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAchR). The sequence includes regions that are conserved throughout the various nAchR alpha subunits and which are essential for ligand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins (AchBERs) and analogues of ligand-gated ion channels, their crystals, and their use for screening ligand-ogated ion channels, their crystals, and their use for screening ligand-ogated ion channels. The water-soluble ligand-binding proteins are capable of channels. The water amenable to crystallization. The crystal structure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and the structure of AChBP is provided that are capable of binding a ligand of a ligand-gated receptor, and comprise at least the amino acids of the AchBP determining solubility of the AChBP, in the same positions as in the achieving solubility of the AChBP, in the same positions as in the chimeric proteins, at least the amino acids of at least to the conserved regions of an nAChR have been substituted for the conserved regions of an nAChR have been substituted in neuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder is Tourette's syndrome,

SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494 453 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494

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                                                                                 4 SPGGVWLALAASLLHVSLQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
                                                                                                            DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                   STYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                    CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
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                                                                  12 APAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                   DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                 Gaps
                                                 70;
nicotine or schizophrenia
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                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
                                  Length
                                                                                                                                                                                                                                                                                                                                              SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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                                Score 1246; DB 4;
Pred. No. 3.1e-115;
5; Mismatches 126;
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addiction to
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                                                 98;
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                                46.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                  Conservative
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Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-061524/07
                                         Similarity
                 502 AA
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                                                  Matches 240;
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Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
                                                                                                                                 The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells
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                                                                                                                                                                                                                                                                                                                                       46.8%; Score 1246; DB 4; I
46.0%; Pred. No. 3.1e-115;
ive 86; Mismatches 126;
                                                                                           Disclosure; Page 61-63; 77pp; English
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                                                                                                                                                                                                                                                                      The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NACARS), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the NACAR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human NACAR (alpha or beta) subunit, such that the cells express an nNACAR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNACAR
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                                                                                                                                                                                             Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
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46.0%; Pred. No. 3.1e-115;
ilve 86; Mismatches 126;
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                                                                                                                                         Harpold MM;
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                                                              90US-00504455.
92US-00938154.
93US-00028031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                    CO INC
                                                                                                                                         Elliott KJ, Ellis SB,
                                                                                                                                                              WPI; 2002-711528/77.
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                                         07-JUN-1995;
                                                                         30-NOV-1992;
08-MAR-1993;
US6440681-B1
                                                                3-APR-1990;
                                                                                              08-NOV-1993;
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hes 240;
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Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             nicotinic acetylcholine receptor; NAChR; drug screening; NAChR alpha7 subunit; receptor.
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453 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM
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46.0%; Pred. No. 3.1e-115;
ive 86; Mismatches 126;
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                                                                                                                                                                                                                                                                                                                                                                                  Human neuronal NAChR alpha7 subunit.
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Matches 240; Conservative
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N-PSDB; ABV73248.
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  251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human neuronal nicotinic acetylcholine receptor nAChR. nAChR's form ligandagted ion channels that mediate synaptic transmissions between nerve and muscle and between neurons upon interaction with the neurotransmitter ecetylcholine. The nucleic acid molecule is useful for identifying compounds that modulate human neuronal nAChR. The present sequence represents the amino acid sequence of the human neuronal nicotinic sectylcholine receptor, nAChR, alpha 7 subunit #1. Note: the present sequence is the sequence encoded by the nAChR alpha 7 subunit DNA ADA10864.
                          DEGGGDISSFVTNGEWELLGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                          CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
                                                                                                                                                                                                                                                                                --VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                                                                                                                                          393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                    MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG------
                                                                                                                                                                                                                                                                                                                            361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human neuronal nicotinic acetylcholine receptor alpha 7 subunit #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha 7 subunit; human; neuronal nicotinic acetylcholine receptor; ligand-gated ion channel; synaptic transmission; gene therapy; transgenic; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEAVCSEWKPAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 67-72; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA10874 standard; protein; 502 AA
                                                                                                                                                                                                                                                                                --SATTPPPAR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                         -DEHLLH
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                                                                                                                             4 SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                     Gaps
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                                                                   70;
                                 502;
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                                                                   Indels
                                   Length
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                             ; Score 1246; DB 7; ; Pred. No. 3.1e-115; 86; Mismatches 126;
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                                 46.8%;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417 -DEHLLH------
                                                  Similarity
Sequence 502 AA;
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                                                                     Matches 240;
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                                 Query Match
                                                        Local
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Costigan M; Befort K, D'urso D, WPI; 2003-268312/26 GENBANK; NP 000737 Woolf C,

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

derivative or allelic variation of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymuclectide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a service so that is differentially expression of the polymuclectide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymuclectide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymuclectides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates the activity of one or more of the polymetication, a method for identifying a compound set in the specification, a method for identifying a compound that regulates the activity of one or more of the polymetic or more of pain and a pharmaceutical composition comprising the one or more polymetides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed specification) but was obtained in electronic form directly from WIPO at specification. invention discloses a composition comprising two or more isolated rat ftp.wipo.int/pub/published pct sequences.

Sequence 502 AA;

241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300 DVDEKNQLLITNIWLKLEMNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131 STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191 -VPPPPDLELRERSSKSLLANVLD 392 DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251 CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVABTMPATSDAVPLLGTYFNCI 311 393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE 452 12 APAGILLILLCLLWPRGARCGYHEKRLLHHILDHYNVLERPVVNESDPLQLSFGLTLMQII 71 4 SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM 63 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----Gaps 312 MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-----101 Length 502; 46.8%; Score 1246; DB 7; Length 5C 46.0%; Pred. No. 3.1e-115; live 86; Mismatches 126; Indels Query Match
Best Local Similarity 46.0%
Matches 240; Conservative 252 72 64 132 192 184 361 qq Dp qq g q δ à ð ò à δ

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	453 DADISRDWKFAAMVVDRLCLIFTLFTIATLAVLLSAPHIM 494	453 SEAVCSEWKFAACVVDRLCLMAFSVFIICTIGILMSAPNFV 494
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Gence 1/USFTO_spool/US09303232/runat_07052004_101110_23883/app_query.fasta_1.2261_08-C9n2_1/USFTO_spool/US09303232/runat_0708-0.1 -LOOPCL=0 -LOOPEXT=0
-DE-CENE 1 - OFWT=fastap -SUPFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-DOCALIGG=200 - TTR SCORE=pct - TTR MAX=100 -TTR MIN=0 -ALIGH=15 -MODE=LOCAL
-OUTFFYT=ptc -NORM=ext -HEAFSIZE=560 -MINIEN=0 -MAXLEN=2000000000
-USER=US09303232_@CGN 1 1_8225_@runat_07052004_101110_23883 -NCFU=6 -ICFU=3
-NO WMAP -LARREQUERY -NEG SCORES=0 -WAIT -DSPBILOK=100 -LONGLOG
-DSW_TIMEOUT=120 -WARN -NIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPDFXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
                                                                                                                 8, 2004, 06:45:49 ; Search time 5459.09 Seconds (without alignments) 3938.047 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                     nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                              3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                       BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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AR173187 Sequence AR224030 Sequence AR282833 Sequence

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AR261850 Sequence BD023656 Variant } AX054567 Sequence Y08420 H.sapiens

AF321446 Drosophil AF321447 Drosophil AF32149 Drosophil BF011147 Drosophil AF321445 Drosophil AF321449 Drosophil AF321449 Drosophil AF33664 Drosophil AF36866 G.gallus mR

AX009610 Sequence AF143847 Heliothis

E58347 Nucleic aci AF272778 Drosophil

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                        AF143846 3629 bp mRNA linear INV 27-MAY-1999 Heliothis virescens putative nicotinic acetylcholine receptor alpha 7-1 subunit mRNA, complete cds.
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7-1 subunit"
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Upublished
2 (bases 1 to 3629)
Schulte,T., Oellers,N. and
Direct Submission
Submitted (19-APR-1999) ZI
51368, Germany
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AUTHORS
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	AX005612 Sequence 3 from Patent EP0962528. AX005612 AX005612.1 GI:9996844 Heliothis virescens (tobacco budworm) Heliothis virescens Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptery Neoptera; Glosaata; Ditryaia	Noctuoidea; Noctuidae; Heliothinae; Heliothis. J. Adamczewski, M.D., Schulte, T.D. and Oellers, N.D. Nucleic acids encoding acetylcholin-receptor subunits Patent: EP 0962528-A 3 08-DEC-1939; BAYER AG [DE] Location/Qualifiers 1. 3700 /organism="Heliothis virescens" /mol_type="unassigned DNA" /db_xref="taxon:7102"	/JOLE="unnamed protein product /codon_start=1 /protein_id="CAC07500.1" /db_xref="G1:996845" (Ab.xref="ERMYRENBL:CAC07500" /translation="MGGRARRSHLAAPAGL XNVLERPVNNESDPLQLSFGITLMQIIUVD GGVKDLRYPPREDRESWTYDGYQLDGL IXYNCCPEPYIDITPAVVIRRKTLYYFFNL VTILLSITYTELNWARTENDAYQLDGL THENSDWIRCYFLYWLPWLENGT THENSDWIRCYFLYWLPWLENGT THENSDWIRCYFLYWLPWLENGT IDDFRHPQAQQPQCCRYYRGGEBNGAGLA	DEDADISRDWKFAAMVUDRLCLIFFLFTIIATLAVLLSABHIMVS OBTIGNA Alignment Scores: 5.99e-247 Length: 3700 Decent Similarity: 100.00\$ Matches: 496 Deser Local Similarity: 100.00\$ Mismatches: 0 Ouery Match: 6 Conservative: 0 Deser Local Similarity: 100.00\$ Mismatches: 0 Ouery Match: 6 Conservative: 0 Ouery Match: 6 Ouery Mismatches: 0 Ouery Match: 6 Ouery Match: 0 Ouery Match: 6 Ouery Mismatches: 0 Ouery Match: 0 Ouery Mismatches: 0 Ouery Mismatches: 0 Ouery Mismatches: 0 Ouery Match: 0 Ouers Mismatches: 0 Ouery Match: 0 Ouers Mismatches: 0 Ouery Mismatches: 0 Ouers Mismatches: 0 Ouers Mismatches: 0 Ouers Mismatches: 0 Ouer

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	ESB147 LOCUS DOCUS BERNATION LOCUS DOCUS DEFINITION DOCIDITION DOCUBLIC acid encoding insect actyl choline receptor subunit. ACCESSION ESB147.1 GI:13019346 KEXPONEDS JO 2000023860-A/2. SOURCE Heliothis virescens Letiothis virescens DOCUGANISM Heliothis virescans DOCUGANISM Neoptera; Endopterayota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Heliothis.	######################################	FH Key Location/Qualifiers (335). (1822). Location/Qualifiers 1. 3701 / organism="Heliothis virescens" /mol_type="genomic DNA" /db_xref="taxon:7102"	Alignment Scores: 5.99e-247 Length: 3701 Score: 2665.00 Matches: 496 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Ouery Match: 100.00% Indels: 0 DB: 6 Gaps: 0	OY 1 MetGlydyArghlaArgArgSerHisLeuAlahlaProAlaGlyLeuLeuLeuLeuLeu 20

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EYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVL
LSAPHIIVS"
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                                                                                                                                                                                                                                                                                                              'note="results in threonine to isoleucine substitution;
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/note="results in asparagine to serine substitution;
compared to B allele"
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/note="results in phenylalanine to
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/replace="a"
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/note="results in serine,
insertion; compared to B a
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NMLSPKTAAATAAGDEATTQQPTNIRLCARKQBLRRRKKKRFATPNETDIKKQQQL
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NNSSTQILNGLNKHSWIFLLIYINLSAKVCLAGYHEKRLHDLLDPYNTLERPVLNES
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TYFAIIRRRTLYYPFNLIIPCVLIASMALLGFTLPPDSGERKISLGYTILLGSLTVFIN
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LCWLPWILRNGRPGREPLILEFPTTPCSGTSSRRKHQILSDVELKERSSKSLLANVLDI
                                                                                                                                                                                                                                                                                                                                       AF272778 2907 bp mRNA linear INV 29-APR-2002
Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5
subunit (nAcRalpha-34E) mRNA, nAcRalpha-34E-A allele, complete cds.
AF272778
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IWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRC
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    TTGGCGCCCACAGTTGCTTCGGTGTCGACTACGAGCTCTCCCTCATTCTGAAGGAGATT 1654
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                     LysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrLeuPheThrIle
                                               ArgValIleThrAspGlnMetArgLysAspAspGluAspAlaAspIleSerArgAspTrp
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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/note="ion channel; neurotransmitter transmembrane
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2907)
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/mol_type="mRNA"
/db_xref="taxon:7227"
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/map="2L; 34E4-5"
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UDRLCIIFTLFTIIATLAVLFSARPFILKELRWITFGQLKKEDFTSDITRDWKFAAMV
 INV 01-APR-2003
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                                                                                                                                   1683 bp mRNA linear .... ... mRNA for nicotinic acetylcholine receptor
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                           AJ554210.1 GI:29466436
nAckalpha-18C gene; nicotinic acetylcholine receptor subunit
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/product="nicotinic acetylcholine receptor subunit
Dalpha7"
                                                                TAGCCACAATAGCTGTACTACTATCAGCACCACATATTATTGTCTCG
                                               481 IlealaThrLeuAlaValLeuLeuSerAlaProHisIleMetValSer
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Mismatches:
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subunit Dalpha7 (nAcRalpha-18C gene).
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organism="Drosophila"
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132. .1651
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AY036613 2834 bp mRNA linear INV 30-APR-2002 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5 subunit (nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds,
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TCCCACACCTGTCTGACATCCTGCGGAGTACGAACTGGGGGCTGATACTCAAGGAGCTG 1471
   TCCGGCGAGAAGAAGCAACAGATCCAAAAGGTTGAGCTCAAGGAGAGGGTCCTCCAAGTCT 1231
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-Co-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                CTGCTGGCCAATGTGCTCGATATAGACGATGATTTCCGATGCAATCATCGATGCCAGC
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Direct Submission
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Submisted (26-MXY-2001) MRC-FGU Human Anatomy and Genetics,
University of Oxford, South Parks Road, Oxford OX1 3QX, UX
Location/Qualifiers
1. c2814
/organism="Drosophila melanogaster"
/mol type="mRNA"
/db zref="mRNA"
/chromosome="2"
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/note="ion channel; neurotransmitter transmembrane
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot
Bobptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/allele="B"
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1 Nucleic acid encoding insect actyl choline receptor subunit.
E58346
E58346.1 GI:13019345
JP 2000023680-A/1.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster.
Enkaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
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                  SerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeuGly
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SMPPFKTRKSTDTYSTPAAITSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWULH
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RIWKPDVLMYRSABGGPGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQR
CEMKFGSWTYDGFQVCPANVTRSITTAARNPI"
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receptor; exon 5 is excluded due to exon skipping, generates a loss of reading frame and a truncated pypeptide, alternatively spliced" foodon start=1 /product="nicotinic acetylcholine receptor Dalpha5
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217 AsnGlulleTyrTyrAsnCysCysProGluProTyrIleAspIleThrPheAlaValVal [1854 AACGAGATCTATTACAACTGCTGCCGGAACCCTATAGACATCACCTCGCCATCGCCATCGCCATCGCCATCGCCATCGCCATCGCCATCGCCATCGCCATCGCCATCGCCATCGCCATCGATCATCATCATCATCATCATCATCATCATCATCATCATCA	Db 2034 GTTACCATCTTGCTCTCGACCGTGTTTTCTGAATATGGTTGCCGAGACAATGCCGGCT 2093 Qy 297 ThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCysIleMetPheMetValAla 316	337 GluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuProTrpValLeuArgMet 2115TGGATACGCATCGTGTTTTTGTGCTGGCTGCCATGGATATTGCGAATG 357 SerArgProGlySerAlaThrThrProProProAlaArgValProProProPro [Qy 375	400ProGlnAlaGlnGlnProGlnCysCysArgTyrTyrArg	0y 423 AlalisSerCysPheGlyValAspTyrGluLeuSerLeuIleLeuLysGluIle 440 2454 CATCALACTGCARCAAATCATCAACTGAATTAGATTAGATTAGATT	Qy 461 LysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrLeuPheThrIle 480 Db 2574 AATTTGCAGCTATGGTCGTTGACAGACTGTGCCTTATCATATTCACAATGTTCGCAATA 2633 Qy 481 IleAlaThrLeuAlaValLeuLeuSerAlaProHisIleMetValSer 496 Db 2634 TTAGCCACAATAGCTGTACTATCGGCACCACATATTATTGTCTCG 2681	RESULT 8 AX009610 LOCUS DEFINITION Sequence 1 from Patent EP0962528. ACCESSION AX009610 VERSION AX009610.1 GI:9996842 KEYWORDS SOURCE DOGGNISM Drosophila melanogaster (fruit fly)
rtin, A. cleic alleic a	FH Acy Location/Qualifiers FT CDS Location/Qualifiers 1. 2886 / Organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227"	Alignment Scores: Pred. No.: Scores: Scores: Scores: 1850.00 Matches: Percent Similarity: 69.96* Mismatches: 69.42* Indels: Owery Match: 69.42* Indels: 75 US-09-303-232-4 (1-496) x E58346 (1-2886)	Qy 17 LeuLeuLeuCysLeuLeuTrpProArgGlyAlaArgCysGlyTyrHisGluLysArg 36	Qy 57 AspProLeuGlnLeuSerPheGlyLeuThrLeumetGlnIleIleAspValAspGluLys 76 Db 1374 GACCGGTTACAATTAAGCTTTAATGCAAATTATCGATGGGACGAGAAA 1433 Qy 77 AsnGlnLeuLeuIleThrAsnIleTrpLeuLysLeuGluTrpAsnAspMetAsnLeuArg 96 Db 1434 AATCAATTGCTACTAATGTGTGGTTAAAACTGGAGTGGAACGACATGAATCTCCGC 1493	Qy 97 TrpAsnThrSerAspheGlyGlyValLysAspLeuArgValProProHisArgLeuTrp 116 Db 1494 TGSAACACCTCCGACTATGGGGAGTTAAGGATCTGGGAATACCGCCGCATCGCATCTGG 1553 QY 117 LysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspSerThrTyrProThr 136 Db 1554 AAGCCGGACTGATGTACAACGATGGGGATTTGACGACTCACCACACGT 1613	eLysser CAAGTCG tLysPhe 	QY 177 GlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnAspGluGlyGlyGly 196 Db 1734 GGCAGTTGGACCTACGACGGATTCCAGCTGGATTTACAATTACAACATGAAACTGGGGGT 1793 QY 197 AspIleSerSerPheValThrAsnGlyGluTrpGluLeuIleGlyValProGlyLysArg 216 Db 1794 GATATCAGCAGTTACGTGCTCAACGGCGAGTGGGAACTACTGGGTGTGCCCGGCAAACGT 1853

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-LeuAla

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2574 AAATTTGCAGCTATGGTCGTTGACAGACTGTGCCTTATCATATTCACAATGTTCGCAATA
                         ACGIGCAAGATCGACATCACGTGGTTCCCCTTCGATGACCAGCGGTGCGAGATGAAGTTC
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                                                                                   GlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGlnAspGluGlyGlyGly
                                                                                                            GGCAGTTGGACCTACGACGGATTCCAGCTGGATTTACAATTACAAGATGAAACTGGCGGT
                                                                                                                                                                         AsplleSerSerPheValThrAsnGlyGluTrpGluLeuIleGlyValProGlyLySArg
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NMLSPKTAAATAAGDEATTQQPTNIRLCARKKQRLBRRRKRRATFBTDIKKQQQL
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NNSSTQILNGLNKHSWIFLLIYINLSAKVCLAGYHEKRLHDLLDPYNTLBRPVLNES
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                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSSTRTTSSNQRH"
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bxapoda; Insecta; Pterygota;
Brachycera; Muscomorpha;
                                                                                   Adamczewski,M.D., Schulte,T.D. and Oellers,N.D.
Nucleic acids encoding acetylcholin-receptor subunits
Patent: EP 0962528-A 1 08-DEC-1999;
BAYER AG (DE)
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/organism="Drosophila melanogaster"
/mol_type="unassigned DNA"
/db_xref="taxon:7227"
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Matches:
Conservative:
Mismatches:
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/note="unnamed protein product"
Eukaryota, Metazoa, Arthropoda, Hexapod
Neoptera, Endopterygota, Diptera, Brach
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                            GGGACCTACCAGACCAACGTGGTGGTGGTCAGAAGCGGCGGCGGTTGCCTGTACGTGCCACCT 514
                                                                                                                                                           CCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGAC 454
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                                                                                                    GACGIGGACGAGAAGAAICAACIAATIAAACCAAIAIAIGGCIGICGIIGGAGIGGAAI
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CDMKFGSWTTJOROQLDLVLKORAGGDLSDFTTNGREWTLIGMFGKKNTITTAACCPEPTV
DVTFTIMITRRRTLYYFFNLIVPCVLISSMALLGFTLEPDSGEKLTLGYTILLSLTYFL
NLVAETLEQVSDA.I PLLGTYFNCINEMVASSVVLTVVVLNYHHRTADIHEMPQWIKSV
FLQWLPWILLRWRSRPGKTITRKTIMMYTRABLELEARBSSKSLLANVLDIDDDERHGGP
PPNSTASTGNLGPGCSIFRTDFRRSEVRESTWEBVGGGGLGSHHRELHILLRELGFITA
RMKKADEERAELISDWKFAAMVUDRFCLFVFTLFTILTATVAVLLSAPHIIVQ"
                                                                                                                                                                                                                                                                                Schulte, T., Oellers, M. and Adamczewski, M.
Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha
                                                                                      27-MAY-1999
                                                                                                    acetylcholine receptor alpha
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Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

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Schulte,T., Oellers,N. and Adamczewski,M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG,
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                                                                                      mRNA
                                                                               AF143847
Heliothis virescens putative nicotinic 7-2 subunit mRNA, complete cds.
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AUTHORS
TITLE
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18	112 ProHisArgLeuTrDLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp 13	212 ValProdiyLysArgAsnGluileTyrTyrAsnCysCysProGluProTyrIleAspIle :::[:::	935 312 995 332 1055 352 1115
		0 A 0 A 0 A 0 A 0 A 0 A	4 6 6 6 6 6
			Alignment Scores: Pred. No.: Pred. No.: 2.4e-164

1175 ACGREGATICAGARACTAGARAGACTTOCTCGATAGATCTTCTCGTCGTCGATAGATCTTTCTCGATAGATCTTCTCGATAGATCTTCTCGATAGATCTTCTCGATAGATCTTCTCTCGTCGATAGTTTCTCTCCTCGATAGTTTCTCTCCTCCTCTCTCT	<pre>ant Similarity: 77.52* Conservative: 55 Local Similarity: 67.05* Mismatches: 78 // Match: 67.88* Indels: 40</pre>	5 AlaArgArgSerHisLeuAlaAlaProAlaGlyLeuLeu	18	32 TyrHisGluLysArgLeuLeuHisHisLeuLeuAspHisTyrAsnValLeuGluArgPro 51	52 ValValasnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleIle 71	72 AspValAspGluLysAsnGlnLeuLeuLeuLethrAsnIleTrpLeuLysLeuGluTrpAsn 91	92 AspMetAsnLeuArgTrpAsnThrSerAspPheGlyGlyValLysAspLeuArgValPro 111	112 ProHisArgLeuTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp 131 	132 SerThrTyrProThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProPro 151	2 GlyllePheLysSerThrCysLysIleAspIleThrTrpPheProPheAspAspGlnArg 	172 CysGluMetLysPheGlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGln 191 :::	192 AspGluGlyGlyGlyAspIleSerSerPheValThrAsnGlyGluTrpGluLeuIleGly 211	212 ValProGlyLysArgAsnGlulleTyrTyrAsnCysCysProGluBroTyrIleAspIle 231 :::		CysValleulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGlu	272 LysLeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAla 291 :::	292 GluThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCysIle 311	2 MetPheMetValAlaSerSerValValSerThrlleLeulleLeuAsnTyrHisHisArg 33
15 ACGAGGA 191 Leuaspi 191 Leuaspi 195 CTAGATA 195 CTAGATA 195 GGGAATT 195 GGGAATT 197 CYCLOGGGGG 191 Prohisi 191 Prohisi	- ertc	yy du	Qy do	Qy da	ZO QZ	Qy Gb	% 8	ζζ Dp	λ	QY	Qy	QY	Qy Dp	QY	op o	Qy	දු ද	δδ
	acgaggatgacggagctgaactgaagagagctcgtcgaagtccttgctgccgaatgtr 123. LeuaspileaspaspasphearghisProglmalaglmgln 404	ProglnCysCysArgTyrTyrArgGlyGly 41	GluGluAsnGlyAlaGlyLeuAlaAlaHisSerCysPheGlyValAsp 430	TyrGluLeuSerLeuIleLeuLysGluIleArgValIleThrAspGlnMetArgLysAsp 450	AspGluAspAlaAspIleSerArgAspTrpiysPheAlaAlaMetValValAspArgLeu 470	CysLeullellePheThrLeuPheThrIlelleAlaThrLeuAlaValLeuLeuSerAla 490	ProHislleMetval 4	3109 bp DNA linear PAT 06-SEP-200 5 from Patent RP0962528	AX009614.1 GI:9996846	got,	om insect	BAYER AG (DE) Location/Qualifiers 13109	5 1 1	/noce="unnamed protein product" /codon_start=1 /protein_id="CAC07501.1" /db_xref="GI:9996847"	/db xref="REWTREMES.CAC07501" /translation="MAPWLAALILIPVSEGGPHEKELLNALLANYNTLERPVANE SEPLEVREGITIQOIIDVDEKNQLLITNIWLSERNDYNIRWDSEYGGYKDLRITPN KIWKEPDVLMAYNSADEGGFGTYQTNIVVRSEGSCLYVPPGITEKSTCKMDIAMFPEDDQH COMMERCEMTYNCANG IN VI KYERYCH STANDYNIRWSEYSTCKMDIAMFPEDDQH	DVTFTIMIRRRTLY FFULLY OVER THE STANDAY IN THE CEPT OF THE STANDAY IN THE STANDAY IN THE STANDAY IN THE STANDAY OF THE STANDAY IN THE STANDAY IN THE STANDAY OF THE STANDAY IN THE STANDAY IN THE STANDAY OF THE STANDAY IN THE STANDAY IN THE STANDAY OF THE STANDAY	RMKKADEEAELISDWKFAAMVURFCLFVFTLFTIIATVAVLLSAPHIIVQ"	: 2.4e-164 Length: 1809.00 Matches:

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variant type II"

'protein id="AAM13393.1"

/db xref="G1:20152847"

/translation="MDSPLPASLSIFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL

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FRFDDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSLTVFLNLVAESMPTTSDAVPLIGTYFNCIMFMVASSVVLTVVVLNYHRTAIHEM
PPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADD
BAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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hore="results in glycine to serine substitution; compared
to variant clone"
/replace="a"
                                                                                                                                                                                                                                                           /codon_start=1
/product="nicotinic acetylcholine receptor Dalpha6 subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession Number AE003626 and in variant clone"
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/note="results in glycine to asparagine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
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                                                                                                                                                                                                               /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b
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  melanogaster"
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'replace="t"
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/replace="t"
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'note="compared to variant clone"
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organism="Drosophila
                                                                                                                                                                                           gene="nAcRalpha-30D"
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                      /mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                       dev stage="embryo" . .2023
                                                               chromosome="2"
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                            995 ATGTTCATGGTAGCGTCGTCTGTGGTACTGACTGTGGTGGTACTCAATTACCACCATCGA 1054
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Wediated A-to-I Per-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK
                                                                                   1055 ACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCA
                                                                                                                             TrpValLeuArgMetSerArgProGlySerAlaThrThrProProAlaArgVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 TyrGluLeuSerLeuIleLeuLysGluIleArgValIleThrAspGlnMetArgLysAsp
                                              HisAlaAspThrHisGluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuPro
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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subunit variant type II
alternatively spliced.
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AF321447
Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type III (nAcRalpha-30D) mRNA, complete cds,
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                                                                                                                                                                                                                                                                                       Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-1 Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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|CGGAAITGAITGGCGGAITGGAAGTTCGCGGCAAITGGTTGTTGAITTTTGTTTAAIT
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                   GlnCysCysArgTyrTyrArgGlyGlyGluGluAsnGlyAlaGlyLeuAlaAla-----
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopteray; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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South Park Road, Oxford
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Submitted (15-NOV-2000) Human Anatomy
Genetics Unit, University of Oxford, S
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/protein_id="AAM13394.1"
/db xref="GI:20152849"
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/organism="Drosophila
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2 (bases 1 to 2023)
Grauso, M. and Sattelle, D.B.
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                                                  ACGCTGGAGCGACCCGTGGCCAATGAATCGGAGCCCCTGGAGGTTAAGTTCGGACTGACG
GAAAGCTGTCAAGGACCTCATGAAAAGCGCCTGCTGAACCATCTGCTGTCCACCTACAAT
                                                                                          LeuMetGlnIleIleAspValAspGluLysAsnGlnLeuLeuIleThrAsnIleTrpLeu
                                                                                                            TCGTTGGAGTGGAACGACTACAATCTGCGCTGGAATGAAACGGAATACGGGGGGTCAAG
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unassatuy 1665 bp mRNA linear INV 01-APR-2003 Brosophila melanogaster mRNA for nicotinic acetylcholine receptor subunit Dalpha6 (nAcRalpha-30D gene).
AJ554209
AJ554209.1 GI:29466434
nACRalpha-30D gene; nicotinic acetylcholine receptor subunit Dalpha6.
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ACAATACTATTAAGCAATGGCATGAAGGGGCTGGAGCTAAAGGAGGGCTCCTCCAAATCC
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|CGGGAATTGATCGGCGATTGGAAGTTCGCGGCAATGGTTGTGGATAGATTTTGTTAATT
 TrpGluLeuIleGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCysProGlu
                 ProTyrIleAspIleThrPheAlaValValIleArgArgLysThrLeuTyrTyrPhePhe
                                                                           AsnLeuIleValProCysValLeuIleAlaSerMetAlaLeuLeuGlyPheThrLeuPro
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/translation="MDSPLPASISTEVILIFIAIIKESCQGPHEKRILNHILSTYNTL
BERVANDSBEPLEVKFGLTIQQIIDVDEKNQLLITULMISIEMNDYNLEWNETEYGGVK
DLRITPNKLWRPDVLMYNSADBGFDFYHTNIVVKHSGSCLYVPPGIFKSTCKNDITW
PPPDDQHCEKKFGSYTYDGNQLDJVLNSEDGGDLSDFITNGFWYLLANFGKKYTIVYA
CCPEPYVDITFIIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
                                                                         LSLTVPLALVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEM 
PWYKSYPLYGALPWILKMRREPRKITHRYTILLSHNRKELELEKRRSSKSLLANVLDIDD 
DFRHTISGSQTARSASSASFGRPTTVBEHHTALGCNHKDLHLILKELQFITARMRKADD 
EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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                                                                                                                                                                                                                                       /gene="nAcRalpha-30D"
/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AB003626"
/replace="a"
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GenBank Accession Number
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Matches:
Conservative:
Mismatches:
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in
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/note="results in glycine
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                               GATCTACGAATCACGCCCAACAAGCTGTGGAAGCCCCGACGTGCTCATGTACAACAGCGCG
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EABLIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLISAPHILIKELQFITTARMRKADD
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Street, London, WCIE 6BT, UNITED
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/product="nicotinic acetylcholine receptor subunit
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/product="nicotinic acetylcholine receptor subunit
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Stableton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Stableton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Glampe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
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1397 GCGGAATTGATCGGCGATTGGAAGTTCGCGGCAATGGTTGTGGATAGATTTTGTTTAATT 1456
                                                                   474 IlePheThrLeuPheThrIleIleAlaThrLeuAlaValLeuLeuSerAlaProHisIle
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-DEC-2003) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                 full insert cDNA.
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GH15518 f
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOR=6 -DELEXT=7
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  4044.486 Million cell updates/sec
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     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                      nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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Searched:

Neuronal Human neu Human neu Alpha 2 s Human neu

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Neuronal Prostate

Chimeric Modified Caenorhab

Drosophil

Human neu Human 205 Human 205 Modified Modified Human CHR Drosophil

Human neu Drosophil Neuronal

Human neu

Neuronal

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds. H. virescens acetyl-choline receptor DNA from clone Hva7-1. /*tag= a /product= "acetyl-choline receptor" AAZ24476 standard; cDNA to mRNA; 3700 BP. Location/Qualifiers 335. .1825 98DE-01019829 98DE-01019829 Heliothis virescens. DE19819829-A1 04-MAY-1998; 04-MAY-1998; 11-NOV-1999 AAZ24476; RESULT 1 AAZ24476 THE SECTION OF SECTION

Oellers N, Schulte T;

(FARB) BAYER AG Adamczewski M,

D. melano H. viresc Drosophil Drosophil Neuronal

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ABL07231 ABL13733 AAT59196 AAV12197 AAT48239

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Aaz24476 H. vireso

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Query Match Length DB

Score

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Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Database

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                                                                                                                                                                                                                     This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (1) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (11). This sequence encodes an acetyl-choline
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                                                                                        New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
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                                                                                                                                                                                                                                                         This invention describes a novel nucleic acid (NA) encoding a nicotinic acety1-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransatission. (1) (also vectors containing it, its regulatory regions, and antibodies protection agents that alter conductance of ACHR, potentially useful as protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (1) are also used to recombinant production of (11). This sequence encodes an acety1-choline receptor isolated from Drosophila melanogaster
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                                        2574 AAATTTGCAGCTATGGTCGTTGACAGACTGTGCCTTATCATATTCACAATGTTCGCAATA 2633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                         TTAGCCACAATAGCTGTACTACTATCGGCACCACATATTATTGTCTCG 2681
                                                                                                                         IlealaThrLeuAlaValLeuLeuSerAlaProHisIleMetValSer 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. virescens acetyl-choline receptor DNA from clone Hva7-2.
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P-PSDB; AAY50816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                    SerHisLeuAlaAlaProAlaGlyLeuLeuLeuLeuCysLeuLeuTrpProArgGly
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321
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Matches:
Conservative:
Mismatches:
Indels:
                                              Sequence 1540 BP; 412 A; 390 C; 376 G; 362
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1623.50
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                                                                       1009 GGACCACTACTACCAGTGTCGAGCAGAAAGCACCTACTTCAATTGCATCATGTTCATGGT
                                                                                      1AlaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArgHisAlaAspTh
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                                        rHisGluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuProTrpValLeuAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
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                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                          detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 ACGAATATTTGGCTCAAATTGGAATGGAACGATATGAATCTTCGATGGAATTCGAGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 LeuAspHisTyrAsnValLeuGluArgProValValAsnGluSerAspProLeuGlnLeu
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                                                                                                                                              + Sequence Listing; English.
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WPI; 2001-656860/75.
P-PSDB; ABB69630.
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                                                                LeuTyrTyrPhePheAsnLeuIleValProCysValLeuIleAlaSerMetAlaLeuLeu
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screen cholinergic agents and other drugs which may affect ligand
binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                 binding protein alpha 1; cholinergic;
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                                AsnCysCysProGluProTyrIleAspIleThrPheAlaValValIleArgA
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2 cDNA clones (AAT59196 and AAT59197) respectively code for the alphal subunit (AAW12368) of chick neuronal alphabungarotoxin binding protein (ABBP). They were isolated from an 18-day embryo chick brain cDNA library using a probe (see also AAT59198) based

English

Claim 1; Fig 2A-B; 18pp;

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on the N-terminal amino acid sequence of chicken brain ABBP. The probe isolated partial clone pGD29-1, which encoded the N-terminal portion of alphal. A subclone, pGD29-3 (ATCC 40641), was used to rescreen the library, yielding clone pGD3-1 (ATCC 40640), which encoded the enrire alpha2 sequence. A probe based on the C-terminal region of pGD3-1 was used obtain clone pCD3-1 (ATCC 40639), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further ABBP subunits, and in the recombinant prodn. of ABBP
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the present sequence encourse a numban necessary and exceptor (NAChR) subunit. The cells expressing the alpha and/or beta naceptor (NAChR) subunit. The cells expressing the alpha and/or beta nach which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with noe or more receptor subtypes indentified e.g. screening with cells that express a variety of subtypes
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                 LeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetProAlaThrSerAspAla
                                                                                                                          ValProLeuLeuGlyThrTyrPheAsnCysIleMetPheMetValAlaSerSerValVal
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 LeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeuGlyValThrlleLeu
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/product= "neuronal nicotinic acetylcholine receptor
alpha-7 subunit"
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                                 SerCysLeuTyrValProProGlyIlePheLysSerThrCysLysIleAspIleThrTrp
                                                                         CATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCGATGTACGCTGG
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                                                                                                                                                                                     GlyGluTrpGluLeuIleGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCys
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GlnMetArgLysAspAspGluAspAlaAspIleSerArgAspTrpLysPheAlaAlaMet
                                                                                        ValValAspArgLeuCysLeuIleIlePheThrLeuPheThrIleIleAlaThrLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
ligand-gated receptor; ds.
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rAla 36	Qy 406 GlnCysCysArgTyTYANgGlyGlyGluGluAsnGlyAlaGlyLeuAlaAlaHisSer 425 Db 1339	194875 standard; cDNA; ABS54875; 06-DEC-2002 (first entr: Human neuronal nicotinic Human; neuronal nicotinic ion flux; alpha 7 subuni; Homo sapiens. Key CDS	FT /*tag= a /*tag= a /*tag= a /*tag= a /*product= "Human nNAChR alpha 7 subunit" XX
Db 1 GGCCGCAGGCCCGGCCGACACCCGAGACGTGGAGCGCCCCGCTCGCT		GINLEUASPLEUGINLEUGINASPGIUGIYGIYGIYASPIIESErSerPheValThrAsn TCCTTGGATCTGCAGATGCAGAGGCAGATATCAGTGGCTATATCCCCAAT GIYGIUTrpGIULeuIIeGIYVAIProGIYLYSARGASBGIUIIETYTTYRASNCYSCYS [265 LeuDroProAspSerGlyGluLySLeuGstleuGlyValThrIleLeuLeuGsrLeuThr 284 832 [

Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to P-PSDB; ABG70492 Identifying

57-60; 56pp; English Claim 101; Col

The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NAVChNS), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human nNAChR polypeptide

T; 0 U; 1 Other; G; 423 530 ΰ BP; 369 A; 553 Sequence 1876

CTGCACGTGTCCCTGCAAGGCGAGTTCCAGAGGAAGCTTTACAAGGAGCTGGTCAAGAAC 180 TrpLeulysLeuGluTrpAsnAspMetAsnLeuArgTrpAsnThrSerAspPheGlyGly 104 $\,$ SerAlaAspGluGlyPheAspSerThrTyrProThrAsnValValValArgAsnAsnGly 144 VallysAspLeuArgValProProHisArgLeuTrpLysProAspValLeuMetTyrAsn 124 ProArgGlyAlaArgCysGlyTyrHisGluLysArgLeuLeuHisHisLeuLeuAspHis 44 LeuThrLeuMetGlnIleIleAspValAspGluLysAsnGlnLeuLeuIleThrAsnIle 84 deccedasececeses de de consecuences de consecue --SerHisLeuAlaAla------ProAlaGlyLeuLeuLeuLeuCysLeuLeuTrp TyrAsnValLeuGluArgProValValAsnGluSerAspProLeuGlnLeuSerPheGly 1876 247 85 129 88 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: (1-1876)US-09-303-232-4 (1-496) x ABS54875 4.91e-115 1247.00 60.47% 44.99% GlyArgAlaArgArg Best Local Similarity: Percent Similarity: Alignment Scores: m 13 61 25 21 45 181 241 65 85 301 105 361 125 421 Query Match: DB: à Dp Dp 8 δ d S S 셤 Q7 Dp qq ਨੇ ð 2 d

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PheProPheAspAspGlnArgCysGluMetLysPheGlySerTrpThrTyrAspGlyTyr 184

GlnLeuAspLeuGlnLeuGlnAspGluGlyGlyGlyAspIleSerSerPheValThrAsn 204

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans.
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note= "neuronal nicotinic acetylcholine receptor"
                                                                                                                 Human; neuronal; nicotinic acetylcholine receptor; NAChR; drug
immunochemistry; NAChR alpha? subunit; gene; ss.
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neuronal nicotinic acetylcholine receptor (nAChR), useful for identifying compounds that modulate human neuronal nAChR activity.
                                                                                          The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human gated ion channels that mediate synaptic transmissions between nerve and muscle and between neurons upon interaction with the neurotransmitter acetylcholine. The nucleic acid molecule is useful for identifying acetylcholine. The nucleic acid molecule is useful for identifying represents DNA encoding the human neuronal nachs. The present sequence receptor, nachs, alpha 7 subunit. Note: the present sequence decodes to the protein shown in ADA10874 not the one described in the specification as being the nachs alpha 7 subunit ADA10865.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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nicotinic acetylcholine
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Best Local Similarity:
                                                         Claim 33; Col
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neuronal
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Thirty PRO polymucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 50; Fig 57; 286pp; English.
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Watanabe CK,
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                                                                                PhePheAsnLeuileValProCysValLeuileAlaSerMetAlaLeuLeuGlyPheThr
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              772 GGCCTCAACCTGCTGATCCCCTGTGTGTGTCTCCGCCCTCGCCCTGCTGTTCCTG
                                                                                                                          LeuProProAspSerGlyGluLysLeuSerLeuGlyValThr1leLeuLeuSerLeuThr
                                                                                                                                     IleLeuAsnTyrHisHisArgHisAlaAspThrHisGluMetSerAspTrpIleArgCys
  GlyGluTrpGluLeuIleGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCys
                                          ProGluProTyrIleAspIleThrPheAlaValValIleArgArgLysThrLeuTyrTyr
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Gurney AL,

Goddard A,

Baker KP, Wood WI;

diagnosis and prevention

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Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glaal disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.
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                                            Human PRO2145 nucleotide sequence SEQ ID NO:76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US012252.
99US-0141037P.
99US-0143048P.
99US-0145698P.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 WO200053755-A2
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02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-2000;
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29-JAN-2001
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO6196, PRO10125, PRO10130, PRO10197, PRO1019

Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;

4.5e-115 1246.00 Alignment Scores: Pred. No.: Score:

AAC58395 standard; cDNA; 1509

AAC58395;

Length: Matches:

Db 961 GACCCCGACGGGGGCCAAGTGGCCCAAGTGGACCAGAGTCATCTTCTGAACTGGTGCGCG 1020 952 TrpValleuargMetSerargProGly	H	QY 370ValProPro 372 Db 1141 AACGGGAACCTGCTGTACATCGGCTTCCGCGGCCTGGACGTGCACTGTGTCCCGACC 1200	QY 373 ProProAspLeuGluLeuArgGluArgSerSerLysSerLeuLeuAlaAsnValLeuAsp 392	Oy 393 IleaspaspaspPheArgHisProGlnAlaGlnGlnProGlnCysCysArgTyrTyrArg 412 :: Db 1249GATGAGCACCTCCTGCAC	Cy 413 GlyGlyGluGluAsnGlyAlaGlyLeuAlaAlaHisSerCysPheGlyValAspTyrGlu 432 :: ::	Cy 433 LeuSerleulleLeuLysGlulleArgValIleThrAspGlnMetArgLysAspAspGlu 452	Qy 453 AspAlaAspIleSerArgAspTrpLysPheAlaAlaMetValValAspArgLeuCysLeu 472 :::	Qy 473 IlellePheThrLeuPheThrIlelleAlaThrLeuAlaValLeuLeuSerAlaPrOHis 492 1117 AIGGCTTCTCGGTCTTCACCATCATCTGCACCATCGGATGTCGGGTGCTCCCAAC 1476	Oy 493 IleMet 494 Db 1477 TTCGIG 1482	RESULT 13 AAC90380 ID AAC90380 standard; cDNA; 1509 BP.	AC AAC30380; XX XX DT 14-MAR-2001 (first entry)	DE Wild-type human alpha7 ligand gated ion channel coding sequence. XX XX Human; alpha7 nicotinic acetylcholine gated ion channel; XW Chydrovytrumtamine. Fum. 2011		PF 25-MAY-2000; 2000WO-US011862. XX PR 27-MAY-1999; 99US-0136174P.	(PHAA) PHARMACIA & UPJ	F. Groppi VE, Wolfe ML, Berkenpas MB; XX DR WPI; 2001-061524/07. DR P-PSDB; AABS0012.	
Percent Similarity: 62.45% Conservative: 86 Best Local Similarity: 45.98% Mismatches: 126 Query Match: 46.75% Indels: 70 DB: 3 Gaps: 6 US-09-303-232-4 (1-496) x AAC58395 (1-1509)	uLeul - 	32 TyrHisGluLysArgLeuLeuHisHisLeuLeuAspHisTyrAsnValLeuGluArgPro 51	leile ::: :::		alPro 		roPro 	lnArg GCAC	euGln 19 :: FGCAG 54	legly ::[]	spile :::						

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cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
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Example 5; Page 60-61; 77pp; English.

The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see ARC90382 and ABS50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells

Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;

•	Oy 1	252 CysValLeulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGlu 271
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	δ,	uAlaAlaHisSerCysPheGlyValAspTyrGlu 432
	qq	1267 GGCGGGCAACCCCCCGAGGGG
	λ	2
	Db	7 Indeccaagancendeadadadacedenacaineceaaregerreegeregeagaedaa 13
	Qy	453 AspAlaAspIleSerArgAspIrpLysPheAlaAlaMetValValAspArgLeuCysLeu 472
	qq	7 AGGAGGGGGTCTGCAGCGAGTGGAAGTTCGCCGCCTGTGTGGTGGACCGCCTGTGCCT
	Qy	473 IleIlePheThrLeuPheThrIleIleAlaThrLeuAlaValLeuLeuSerAlaProHis 492
	Db	greddereceaa
	۵۲	493 IleMet 494
	Db	1477 TTCGTG 1482
	RESULT 1- AAV44687 ID AAV	4 44687 standard; cDNA; 1590 BP.
	AC AAV	
	60	-OCT-1998 (first entry)
	DE V27	4T variant human alpha? nAChR coding sequence.
	KW Alpha7 KW neurod	na7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; codegeneration; enzyme dysfunction; affective disorder; therapy; ne dysfunction; diabetic neuropathy; Alzheimer's disease;
		dystmiccion; arabetic metopacit, introcessor

GACGIGGAIGAGAAGCAAGTITIAACCACCAACAITIGGCIGCAAAIGICTIGGACA 257

198

258

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92

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ASPMetasnleuargTrpasnThrSeraspPheGlyGlyValLysaspLeuargValPro

ProHisArgLeuTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp 131

GATGGCCAGATTTGGAAACCAGACATTCTTCTCTATAACAGTGCTGATGAGGCCTTTGAC

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                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes the V247T variant of human alpha7 nicotinic acetylcholine receptor (nAchR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify medulators of alpha7 nAchR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurogeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru, by sychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while emonclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAchR, the protein has about 100-fold greater sensitivity to cholineragic receptor agonists diceine or acetylcholine) and response to these
                                                                                                                                                                                                                                                                                                   Nucleic acid encoding variant of human alpha 7 nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer etc.
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                                                   Location/Qualifiers
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Sullivan JP,
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GAGTICCAGAGGAAGCITIACAAGGAGCIGGICAAGAACIACAATCCCIIGGAGAGGCCC 137 77 51 ValValAsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleIle 71 31 AspValAspGluLysAsnGlnLeuLeulleThrAsnIleTrpLeuLysLeuGluTrpAsn 91 TyrHisGluLysArgLeuLeuHisHisLeuLeuAspHisTyrAsnValLeuGluArgPro AGCCCCGGAGGAGTGTGGCTGGCACTGGCAGCATCTCTCCTGCACGTGTCCCTGCAAGGC BP; 322 A; 471 C; 449 G; 348 T; 0 U; 0 Other; 1590 239 86 127 70 Length: Matches: Conservative: Mismatches: Indels: Gaps: (1-1590)x AAV44687 1.23e-114 1242.00 62.26% 45.79% 46.60% US-09-303-232-4 (1-496) Percent Similarity: Best Local Similarity: Sequence 1590 Alignment Scores: 12 18 32 78 25 138 72 Best Local : Query Match δ g 원 ₽ 원 δ ò

231 1274 SerThrTyrProThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProPro 151 437 GlyllePheLysSerThrCysLyslleAspIleThrTrpPheProPheAspAspGlnArg 171 191 557 211 608 668 728 788 251 271 848 291 GluThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCysIle 311 MetPheMetValAlaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArg 331 --ValProPro 372 CysGluMetLysPheGlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGln ValProGlyLysArgAsnGluIleTyrTyrAsnCysCysProGluProTyrIleAspIle 609 ATCCCCGGCAAGAGGTGGAAAGGTTCTATGAGTGCTGCAAAGAGCCCTACCCCGATGTC ThrPheAlaValValIleArgArgLysThrLeuTyrTyrPhePheAsnLeu1leValPro CysValLeuIleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGlu 192 AspGluGlyGlyAspIleSerSerPheValThrAsnGlyGluTrpGluLeulleGly GAG------GCAGATATCAGTGGCTATATCCCCAATGGAGAATGGGACCTAGTGGGA ACCTTCACAGTGACCATGGGCGCCGCAGGACACTCTACTATGGCCTCAACCTGCTGATCCCC LysLeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAla HisAlaAspThrHisGluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuPro 393 IleAspAspAspPheArgHisProGlnAlaGlnGlnProGlnCysCysArgTyrTyrArg .029 ridentocricida Arida Adadecocidada Adada Caraca Consecratora Cons --SerAlaThrThrProProProAlaArg 1149 AACGGGAACCIGCIGIACAICGGCIIICCGCGGCCIGGACGGCGIGCACIGIGIACCGGACC ProProAspLeuGluLeuArgGluArgSerSerLysSerLeuLeuAlaAsnValLeuAsp .209 cccarcresesras de rerescence en consecue en conse TrpValLeuArgMetSerArgProGly 1257 ---ĠArGAGCACCTCCTGCAC---132 378 152 438 498 212 172 558 232 699 252 729 272 789 292 849 312 606 332 696 373 352 361 a ద δ E E à d à В à g ò 염 à

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
                                                                                                                                                                       452
                                                                                                           472
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                 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline
              GlyGlyGluGluAsnGlyAlaGlyLeuAlaAlaHisSerCysPheGlyValAspTyrGlu
                                                                           --GACCCGGAC
                                                                                                                            473 IleIlePheThrLeuPheThrIleIleAlaThrLeuAlaValLeuLeuSerAlaProHis
                                                                                                             453 AspAlaAspIleSerArgAspTrpLysPheAlaAlaMetValValAspArgLeuCysLeu
                                                              LeuSerLeulleLeuLysGlulleArgVallleThrAspGlnMetArgLysAspAspGlu
                                                                                                                                                                                                                                                                                                                                                                       Human; alpha7 nicotinic acetylcholine gated ion channel; mutant; 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
                                                                                                                                                                                                                                                                                                                                                  Mutant human alpha7 ligand gated ion channel coding sequence #1.
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                                       1275 GGCGGCAACCCCCCGAGGGG-
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P-PSDB; AAB50015.
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352 TrpValLeuArgMetSerArgProGly360	1021 TGGTTCCTGCGAATGAAGAGCCCGGGGAGGACAAAGGTGCGCCCGGCCTGCCAGCACAAG 1080	361	1081 CAGCGGCGCTGCAGCCTGGCCAGTGTGGAGATGAGCGCCGTGGCGCCGCCGCCGCCAGC 1140	370ValProPro 372	 1141 AACGGGAACCTGTACATCGGCTTCCGCGGCCTGGACGGCGTGCACTGTGTCCCGACC 1200	373 ProProAspLeuGluLeuArgGluArgSerSerLysSerLeuLeuAlaAsnValLeuAsp 392	01 CCCGRCTCTGGGGTAGTGTGTGCCCGCATGGCCTGCTCCCCCACGCAC 1248	393 IleAspAspAspPheArgHisProGlnAlaGlnGlnProGlnCysCysArgTyrTyrArg 412	1249GATGAGCACCTCCTGCAC 1266	413 GlyGlyGluGluAsnGlyAlaGlyLeuAlaAlaHisSerCysPheGlyValAspTyrGlu 432		433 LeuSerLeuIleLeuLysGluIleArgValileThrAspGlnMetArgLysAspAspGlu 452	::: :: :: 97 TIGGCCAAGAICCIGGAGGAGGICCGCIACAIIGCCAAICGCTICCGCIGCCAGGACGAA 1356	453 AspAlaAspIleSerArgAspTrpLysPheAlaAlaMetValValAspArgLeuCysLeu 472		473 IleIlePheThrLeuPheThrIleIleAlaThrLeuAlaValLeuLeuSerAlaProHis 492	iii	493 IleMet 494	::: 1477 TTCGTG 1482	
Qy 3	Db 10	Q <i>y</i> 3	Db 10	3.	Db 11.	3,	Db 1201	33	Db 124	Qy 4.1	Db 1267	Оу 4	Db 1297	Qy 45	Db 135	Qy 4.7	Db 141	Qy 4.5	Db 147	

Search completed: May 8, 2004, 19:30:17 Job time : 553.982 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

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7, 2004, 11:31:03 ; Search time 12.0702 Seconds (without alignments) 3952.801 Million cell updates/sec

US-09-303-232-4

2665 1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHIMVS 496 Perfect score:

Sequence:

Scoring table:

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Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Listing first 45 summaries

PIR 78:*
1: pir1:*
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æ	Query Match	47.5	46.6	46.6	46.6	46.2	45.8	45.1	42.8	39.8	39.6	36.7	36.1	36.0	35.9	35.8	35.8	35.1	35.0	34.7	34.5	34.1	٠	33.9	•	•	33.8	33.8	33.7	33.7
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495	457	200	457	457	470	445	457	517	459	627	457	468	521	625	565
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898	896.5	892.5	890	889	888	887	886	886	885.5	879.5	876.5	875.5	875	874	869
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 NO013 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken NyAlternate names: alpha-bungarotoxin-binding protein alpha chain Cispecies: Gallus gallus (chicken)
R;Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.; Neuron 5, 847-856, 1990
A,Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmental. A,Reference number: JN0113; MUID:91097796; PMID:1702646

A;Accession: JN0113
A;Molecule type: DNA
A;Residues: 1-502 <COU>
A;Residues: 1-502 <COU>
A;Cross-references: GB:X68586; NID:g287756; PIDN:CAA48576.1; PID:g287757
A;Experimental source: white leghorn; brain
R;Schoepferr, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990

Neuron 5, 35-48, 1990 A/Title: Brain alpha-bungarotoxin binding protein CDNAs and MAbs reveal subtypes of thim A/Reference number: JH0172, MUID:90315158; PMID:2369519 A, Accession: JH0172

A; Molecule type: mRNA A; Residues: 1-502 <SCH> A; Residues: 1-502 <SCH> A; Residues: 1-502 <SCH> A; Cross-references: EMBL:X52295; NID:963077; PIDN:CAA36543.1; PID:963078 A; Experimental source: brain B; Matter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M. EMBO J. 11, 4529-4538, 1992 A; Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter de A; Reference number: \$28018; MUID:93049204; PMID:1425587

A; Accession: 228018
A; Molecule type: DNA
A; Residues: 1.18 c.MSS.
A; Residues: 1.18 c.MSS.
A; Experimental source: white leghorn; erythrocyte
A; Experimental source: white leghorn; erythrocyte
B; Conti-Tronconi, B.M.; Dunn, S.M.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; Ra
A; Title: Brain and muscle nicotinic acetylcholine receptors are different but homologous
A; Reference number: A94055; MUID:85270494; PMID:3860855
A; Accession: B25738
A; Molecule type: protein
A; Residues: 24-25, ET', 28-41, X', 43-45, X', 47 < CON>
C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized

Aintrons: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
Cisuperfamily: acetylcholine receptor
Cisuperfamily: acetylcholine receptor
Cisyportenin; glycoprotein; on channel; neurotransmitter receptor; phosphoprotein;
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted *SIG>
F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted *IRI>
F;21-224/Domain: transmembrane #status predicted <IRI>
F;262-280/Domain: transmembrane #status predicted <IRI>
F;296-317/Domain: transmembrane #status predicted <IRA>

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F;46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F;365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted F;415/Binding site: phosphate (Thr) (covalent) #status predicted F;442/Binding site: phosphate (Tyr) (covalent) #status predicted
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C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-Aug-1999
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                                                                                                                                        1 MGGRARRSHLAAPAGLILLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
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                                                                                 Length 502;
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
C;Accession: G02259
R;Leonard, S.
submitted to the EMBL Data Library, November 1995
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                                                                                                             83; Mismatches 144; Indels
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46.0%; Pred. No. 2.6e-100;
cive 84; Mismatches 128;
                                                                               47.5%; Score 1267; DB 2;
48.6%; Pred. No. 1.7e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Reference number: H00936
A,Accession: G02259
A,Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-502 <LEO>
                                                                                              Best Local Similarity
Matches 249; Conserv
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Best Local Si
Matches 240;
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A;Reference number: 137185; MUID:94195283; PMID:8145738
A;Accession: 137185
A;Accession: 137185
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A;Residues type: mRNA
A;Residues: 1-502 <PENA:
A;Cross-references: Drain neuroblastoma cell line SHSY-5Y
A;Cross-references: Drain neuroblastoma cell line SHSY-5Y
B;Chini, B; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.
A;Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic
A;Reference number: A54194; MUID:94245214; PMID:8188270
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A; Gross-references: GDB:138751; OMIM:118511
A; Gross-reference: Gross-receptor molecule is a heteropentamer with two alpha chains a c; Complex: the functional receptor molecule is a heteropentamer with two alpha chains a c; Complex: the functional receptor molecule is a heteropentamer with two alpha chains a cycloprotein; heteropentamer; ion channel; neurotransmitter receptor F; 1-23/Domain: signal sequence #status predicted <SIG>F; 22-280/Domain: transmembrane #status predicted <TR1>F; 22-280/Domain: transmembrane #status predicted <TR2>F; 26-380/Domain: transmembrane #status predicted <TR2>F; 26-380/Domain: transmembrane #status predicted <TR3>F; 40,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999
C;Accession: 137185; A54194; S60309
R;Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, S46-554, 1994
A;Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
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A,Molecule type: mRNA
A,Residues: 24-363,'8',355-374','A',376-408,'AWPAP',414-502 <CHI>A,Cross-references: GB:Z23141; NID:g457736; PIDN:CAA80672.1; PID:g457737
A,Experimental source: retina
C,Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and
                                       301 MIIVGLSVVVTVIVIQYHHHDPPGGKMPKWTRVILLNWCAWFLRWKRPGEDKVRPACQHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human N;Alternate names: cholinergic nicotinate receptor alpha-7 chain
STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                           DEGGGDISSFVINGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
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Cispecies: Rattus norvegicus (Commay rat)
Cispecies: Rattus norvegicus (Commay rat)
Cispecies: Rattus norvegicus (Commay rat)
Cispecies: 103, 996-604, 1993
A; Neurosci: 13, 596-604, 1993
A; Neurosci: 13, 596-604, 1993
A; Neurosci: 13, 596-604, 1993
A; Neterence number: 214310; MUD:93147931; PMID:7678857
A; Reference number: 214310; MUD:93147931; PMID:7678857
A; Reference number: 214310; MUD:93147931; PMID:7678857
A; Reference number: 214310; MUD:93147931; PMID:368857
A; Residues: 1502 <8859
A; Residues: 1-502 <8859
A; Cross-references: EMBL:853987; NID:9264770; PIDN:AABE55224.2; PID:95705903
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                                          Query Match 46.6%; Score 1241; DB 2; Best Local Similarity 47.1%; Pred. No. 3.2e-100; Matches 243; Conservative 90; Mismatches 139;
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47.2%; Pred. No. 1.8e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ENGAGLAAHSCFGV---
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Matches 244; Conservative
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Dioctinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
C; Species: Mus musculus (house mouse)
C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
C; Accession: A57175

R; Orr-Untreager, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
Genomics 26, 399-402, 1995
A; Title: Cloining and mapping of the mouse alpha7-neuronal nicotinic acetylcholine recept
A; Reference number: A57175; MUID: 95324936; PMID: 7601470
A; Recession: A57175
A; Status: preliminary
A; Modession: A57175
A; Status: predicted ATR2>
A; Cross-references: GB: L37663; NID: 9790853; PIDN: AAC42053.1; PID: 9790854
C; Superfamily: acetylcholine receptor alpha-7 chain, neuronal #status predicted ATR2>
F; 26-280/Domain: transmembrane #status predicted ATR3>
F; 26-280/Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251
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                                                                                                                                                                                                                                                                                                                               SPGGVWLGLAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST
                                                                                                                                                                                                                                                                        12 APAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLOLSFGLTLMOII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 IDDDFRHPQAQQPQCCRYYRGGBENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                    Gaps
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F;150-164/Disulfide bonds: #status predicted
F;365,413/Binding site: phosphate (Ser) (covalent) #status predicted
F;415/Binding site: phosphate (Thr) (covalent) #status predicted
F;442/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                              70;
                                                                                                                                                                                                                 86; Mismatches 126; Indels
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                                                                                                                                                        Score 1241; DB 1;
Pred. No. 3.2e-100;
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                                                                                                                                                  46.6%;
                                                                                                                                                                                                              Matches 240; Conservative
                                                                                                                                                                                Similarity
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                                                                                                                                                        Query Match
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	8 6 8 6 8 6 8 6 8	193ADISNYISNGEWDLVGVPGKRNELYYECCKEPYPDVTYTITMRRRTLYYGLNLLIPC 249 253 VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIM 312
ASS RDWKFAAMVVDRLCLIFTLFTIATLAVLLSAPHIM 494 1	RESULT 7 568588 nicotinic acet C;Species: Cae C;Date: 06-De C;Date: 06-De C;Accession: 6 A;Title: Nicot A;Reference A;Reference A;Reference A;Reference A;Reference A;Reference A;Residues: 1. A;Residues	RESULT 7 568588 nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999 C;Accession: 686888; 557496 B;Ballivet, M; Alliod, C; Betrrand, S; Bertrand, D. J. Mol. Biol. 258, 261-269, 1996 A;Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans. A;Reference number: 568587; MUD:96196478; PMID:8627624 A;Recession: 568588 A;Accession: 568588 A;Accession: 568588 A;Accession: 568588 A;Accession: 568588 A;Accession: 568588 A;Accession: 568588 A;Cross-references: EMBL:X83887; NID:9872087; PIDN:CAA58764.1; PID:9872088 C;Superfamily: acetylcholine receptor C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane F;1-19/Domain: signal sequence #status predicted <agt #status="" <amt="" acetylcholi<="" acetylcholine="" actinic="" alpha-1="" c;cores-reference="" c;superfamily:="" chain="" cores-reference="" predicted="" receptor="" td=""></agt>
2 ch	\$ 60 \$ 60 \$ 60 \$ 60 \$ 60 \$ 60 \$ 60 \$ 60	LLLCCLLWPRGARCGYHEKELLHHLLDHYNVLERPVVNBSDPLQLSFGLTLMQIIDVDEK :
<pre>Query Match Query Match Best Local Similarity 46.3%; Pred. No. 2.5e-98; Matches 236; Conservative 88; Mismatches 131; Indels 55; Gaps 9; 20 LCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIID 72 </pre>	os os os	137 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWIYDGYQLDLQLQDBGGG 196
73 VDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDS 132	oy oy oy	257 SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNRVAETMPATSDAVPLLGTYFNCIMFWVA 316 [
193 EGGGDISSFVTNGEWELIGVPGKRNEIVYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPC 252	ζζ	373 PPDLELRERSSKSLLANVLDIDDFRHPQAQQPQC-CRYYRGGEENGAGLAA 423 : : : : : : :

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Similarity
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hes 217; (
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Best Local S
Matches 217
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                                                                                                                                                                                   RESULT 8
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T25671
R;Gattung, S.; Maggi, L.
Submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid D2092.
A;Reference number: Z20067
A;Accession: T25671
A;Accession: T25671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-461 - GAT>
A;Residues: 1-461 - GAT>
A;Residues: Sexion: T2660- GAT>
A;Cross-references: EMBL:U88167; PIDN:AAB42223.1; GSPDB:GN00019; CESP:D2092.3
A;Experimental source: strain Bristol N2; clone D2092
C;Genetics: CFGD-1000-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
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                                                   418 ISSNGTTTDVSQQATLLILHRIYHELKIVTKRMIEGBKEEQACNNWKFAAMVVDRLCLYV 477
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-----NRHSESLIRNIKDNEHSLSRANSFDADCRLNQYIMTQSVSNGLTSLGSIPSTM 417
                               HSCFGVDYELS----LIL----KEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLII 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 NIRWNTSDFGGVKDLRVP--PHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 EKRLIHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
A;Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C;Superfamily: acetylcholine receptor
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                                                                                                    FTLFTIIATLAVLLSAPHIM 494
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FTIFIIVSTIGIFWSAPYLV 497
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Best Local Similarity 46.2
Matches 218; Conservative
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T19622
R;Kershaw, J: 19622
R;Kershaw, J: Submitted to the EMBL Data Library, April 1997
A;Reference number: 219153
A;Reference number: 219153
A;Residues: T19622
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-560 < WILD>
A;Experimental source: Glone C31H5
C;Genetics: A;Gene: CESP:C31H5.3
A;Map position: 1
A;Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C;Superfamily: acetylcholine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 YFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 LGTYFNCIMFMVASSVVSTILILNYHHRHADTHE-MSDWIRCVFLYWLPWVLRMSRPGSA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
R;Hembry, C.
submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 -----INTTISPATYKPNGEWELLGITSQRSIFFYECCPEPYYDVTFTVSIRRRILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 YGFNLLLPCMLISSLALLSFTLPADCGEKINLGVTIFMSLCVFMIMVAEAMPQTSDALPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ILLILICLINPRGARC-----GYHEKRLIHHILDHYNVLERPVVNESDPLQLSFGLTLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 IIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 FDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 FDSTWPVNAVVLYTGNVTWIPPAIIRSSCAIDIAYFPFDTQHCTWKFGSWTYSGFFTDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 LQDEGGGDISSFVT-----NGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCRYYRGGEENGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 DLSTGNPHSDAKKSSPSPKRTSASIMGMTGLPTTQMNGALDSSINKYTCTKVTRPLENGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.8%; Score 1060; DB 2; ilarity 37.6%; Pred. No. 2.4e-84; Conservative 96; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -RERSSKSLLANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 DWMFASRVVDRVCFLAFSAFLFMCTAIISYNAPHLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 DIDDDFRHPQAQQPQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTPPPARVPPPPDLEL
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A; Accession: T19862

T19622 hypothetical protein C31H5.3 - Caenorhabditis elegans

11;

10;

Gaps

78;

70 63

183 188

242

362

357

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243 YYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RQLLADLASKRLIRHAHNSKISAAAAAAAASSSAASSPDSLRHHH 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFELEKAIHNVLFIQNHMQRQDEFDAE-DQDWGFVAMVLDRLFLWIFTIASIVGTFAILC 527
                                                                                                                                                                                                                                                                                                                           64 IDLNLKDQILTTNVWLEHEWQDHKFRWDPAEYGGVTELYVPSEHIWLPDIVLYNNADGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                     124 VVITMIKAVLHHIGKVVWIPPALFKSSCEIDVRYFPFDQQICFMKFGSWIYDGDQIDLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSA
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                                                                                                                                                                                        11 AAPAGLLILLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQI
                                                                                                                                                                                                                            4 ALPPMLILILILILIHHPAAANPDAKRLYDDLLSNYNRLIRPVSNNTDTVLVKLGLRLSQL
                                                                                                                                                                                                                                                                                               71 IDVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGF
                                                                                                                                                                                                                                                                                                                                                                                                         131 DSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --QLQDEG----GGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 FYIVNLIVPCVGISYLSVLVFYLPADSGEKIALCISILLSQTMFFLLISEIIPSTSLALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 LHQHQHHLQLHHLQRPGGCNGLHSATNRFGGSAGAFGGLPSVVGLDGSLSDVATRKKY
F;501-523/Domain: transmembrane #status predicted <TM4>
F;47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                              ; Score 979; DB 2; Length 55; Pred. No. 2.8e-77; 88; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 AQQPQCCRY----YRGGEENGAGLAAH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTPPPARVPPPDLELRERSSKSLL
                                                                                36.7%;
40.0%;
                                                                                                                                      Conservative
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A; Reference number: S21338
                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAP 491
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                                                                           Query Match
Best Local Simil
Matches 217; (
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C;Species: Schistocerca gregaria (desert locust)
C;Species: Schistocerca gregaria (desert locust)
C;Species: 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: 512359
C;Accession: 612359
C;Acce
                                                                                                                                                                                                                    4
                                                                                                                                                                             A,Map position: X
A,Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;
C,Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLL-----GTYFNCIMFMVASS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITD 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRVTYSKVMAESYVEDVVMTELNKYMQ-----KACL---ELKNISSQTRAMRK 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---PQAQQ 404
                      A; Molecule type: DNA
A; Residues: 1-542 <WILD>
A; Cross-references: EMBL: Z70266; PIDN: CAA94206.1; GSPDB: GN00028; CESP: C40C9.2
A; Experimental source: clone C40C9
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                  210 GEWNLLAVPARHETNIFD--EQPYPSLFFYLIIQRRTLYYGLNLIIPSFLISLMTVLGFT
                                                                                                                                                                                                                                                                                                                                                                                                    EKRLIHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLRWNTSDFGGVKDLRVP--PHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ-----DEGGGDISSFVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFT
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                    85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RV-----PPPPDLELRERSSKSLLANV-----LDIDDDF--RH---
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                          39.6%; Score 1055.5; DB 2;
40.5%; Pred. No. 5.6e-84;
tive 94; Mismatches 136;
preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.5%
Matches 214; Conservative
                                                                                                                                                      A, Gene: CESP: C40C9.2
                                                                                                                                                                                                                                                                                                                                                                                                    34
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430

----SCFGVD-----

401

ANVLDIDDDFRHPQ

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the alpha3 subunit of a neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of the mature human nicotinic acetylcholine receptor
                           C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C;Accession: A55956; S21338
R;Mihovilovic, M.; Roses, D.
Exp. Neurol. 111, 175-180, 1991
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit cA;Reference number: A53956; MUID:91114756; PMID:1989896
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
                                                                                                                                                                                                                                                                                           A, Accession: A53956
A, Status: preliminary
A, Molecule type: mRNA
A, Ressidues: 1-503 < MIH>
A, Cross-references: GB: M37981; NID: g189252; PIDN: AAA59942.1; PID: g189253
R, Anand, R.; Lindstrom, J.
submitted to the EMBL Data Library, June 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 30-503 <ANA>
A;Cross-treferences: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C;Genetics:
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C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted <3
F;2-2-240/Domain: extracellular #status predicted <EXI>F;22-240/Domain: transmembrane #status predicted <EXI>F;270-264/Domain: transmembrane #status predicted <TM1>
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A,Molecule type: DNA
A,Residues: 1-57 < AGOS>
A,Cross-references: GB:X07194; NID:97575; PIDN:CAA30172.1; ]
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C; Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Conservation of neural nicotinic acetylcholine A,Reference number: S00381; MUID:88283626; PMID:2840281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: FlyBase:nAcR-alpha-96Aa
A,Cross-references: FlyBase:FBgn0000036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: 538-Tyr was also found
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A, Molecule type: mRNA
A, Residues: 1-567 <BO2>
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A; Introns: 64/3; 79/3;
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C;Species: Gallus gallus (chicken)
C;Daces: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: 800377
R;Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
A;Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
A;Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylchd
A;Reference number: 800376; MUID:88283624; PMID:3267226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Superfamily: acetylcholine receptor
C,Superfamily: acetylcholine receptor
C,Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-52/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <MAT>
F;24-26/Domain: transmembrane #status predicted <TM1>
F;202-290/Domain: transmembrane #status predicted <TM3>
F;502-220/Domain: transmembrane #status predicted <TM4>
F;502-220/Domain: transmembrane #status predicted <TM4>
F;54,104/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;158-172,222-223/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 EYLLFTMIFVTLSIVITVFVLNVHYRTPTTHTMPSWVKTVFLNLLPRVMFMTRPTSNEGN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 FNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 INLIIPCLLISFLTVLVFYLPSDCGEKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
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                                                                                                                                                                                                                                                                                                                                                 126 ADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                              125 AVGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWSYDKAK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 AOKPRPLYGAELSNLNCFSRAESKGCKEG-----YP-CODGMCGYCHHRRIKISNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ILKEIRVITDOMRKDDEDADISRDWKFAAMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S00377
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-528 <NEF>
A;Cross-references: EMBL:X07339; NID:g62792; PIDN:CAB59645.1; PID:g6136914
C;Genetics:
A;Introns: 21/1; 73/3; 88/3; 125/2; 487/3
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                                                                                                                                                                                                                    10 LAAPAG----LLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGL
                                                                                                                                                                                                                                                                LAAPGAVAPRLILLILISILP-VARASEAEHRLFERLFEDYNEIIRPVANVSDPVIIHFEV
                                                                                                                                                                   Gaps
                                                                                                                                                                   34;
                                                                                                               Length 503;
                                                                                                                                                                   89; Mismatches 172; Indels
                                                                                                                  36.1%; Score 962; DB 2; 41.1%; Pred. No. 7.3e-76;
A; Cross-references: GDB:125219; OMIM:118503
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                  A,Map position: 15q24-15q24
C,Superfamily: acetylcholine receptor
C,Keywords: neurotransmitter receptor
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                                                                                                                                                                        206; Conservative
                                                                                                                  Query Match
Best Local Similarity
Matches 206; Conserv
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                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                               NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                 PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
                                                                                                                                                                                                                                                     211 GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                                               -- PPPDLELRERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 RSPSTHTWPHWVRSFFLGFIPRWLFMKR-----PPLLLPAEGTTGQYDPFGTRL--ST
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                                                                             GYHEKRILLHHILDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
                                                                                                                                                                                           SDYKLRWNPEDFDNVTSIRVPSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSNGKVKWVP
                                       Gaps
                                         62;
   Length 528;
36.0%; Score 959; DB 1; Length 52
39.2%; Pred. No. 1.4e-75;
:ive 84; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 RHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP
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Best Local Similarity 39.2%
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R;Pornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
Neurosci. Lett. 111, 351-356, 1990
Neurosci. Lett. 111, 351-356, 1990
A;Title: Molecular cloning of human neuronal nicotinic receptor alpha-3-subunit.
A;Reference number: A37040; MUID:90245296; PMID:2336208
A;Rocession: A37040; MUID:90245296; PMID:2336208
A;Rocession: A37040
A;Rocession: A37040
A;Rocession: A57040
A;Rosidues: 1-502 *PORA
A;Residues: 1-502 *PORA
A;Residues: 1-502 *PORA
A;Residues: 1-502 *PORA
C;Superfamily: acetylcholine receptor; transmembrane protein
C;Reywords: neurotransmitter receptor; transmembrane protein
F;1-28/Domain: signal sequence #status predicted <SIG>F;29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <
                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                    192
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C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
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VFIALHFATGGLANPDAKRLYDDLLSNYNRLIRPVGNNSÜRLTVKMGLRLSÖLIDVNLKN
                                                                                                                                                                                                                                                                             QLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTN
                                                                                                                                                                                                                                                                                                                                                     138 VVVRNNGSCLYVPPGIFKSTCKIDITWPPFDDQRCEMKFGSWTYDGYQLDL----QLQD-
                                                                                                                                                                                                                                                                                                                                                                              129 AILHHTGKVVWKPPAIXKSFCEIDVEYFPFDEQTCFMKFGSWTYDGYMVDLRHLKQTADS
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                                                                                                                                                               Gaps
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                                                          predicted
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40.8%; Pred. No. 3.6e-75;
Live 90; Mismatches 174; Indels 30;
                                                                                                                    Length 567;
                                                                                                                                                             Indels
              F;326-513/Domain: intracellular #status predicted <INT>
F;514-523/Domain: transmembrane #status predicted <TM4>
F;45,233/Binding site: carbohydrate (Asn) (covalent) #status
F;149-163,222-223/Disulfide bonds: #status predicted
;306-325/Domain: transmembrane #status predicted <TM3>
                                                                                                                 Score 957.5; DB 1;
Pred. No. 2.1e-75;
5; Mismatches 174;
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                                                                                                           35.9%; Scor
38.2%; Pred
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Best Local Similarity 40.8%
Matches 203; Conservative
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Matches 206; Conservative
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IIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG 129
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                                                                                                                                                                           190 LQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLI
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search completed: May 7, 2004, 11:39:31 Tob time: 13.0702 secs Ч

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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 7, 2004, 11:18:28 ; Search time 9.26316 Seconds (without alignments) 2788.120 Million cell updates/sec Run on:

US-09-303-232-4 2665 1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHINVS 496 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES Re

	ption	P22770 gallus gall		P49582 mus musculu		P54131 bos taurus		P91766 manduca sex	schis	P32297 homo sapien	Q15822 homo sapien	P09480 gallus gall	P09478 drosophila	P12389 rattus norv		ratt	dros	gall	Q15825 homo sapien	gall		P02711 torpedo mar	-	P30926 homo sapien	P17787 homo sapien		P02710 torpedo cal	P18845 carassius a		P02709 bos taurus		P25162 drosophila	80	156
SUMMARIES	ID	ACH7 CHICK	ACH7_HUMAN	ACH7 MOUSE	ACH7_RAT		ACH1_CAEEL				ACH2_HUMAN	ACH2_CHICK	ACH1_DROME	ACH2_RAT	ACH3 BOVIN	ACH3_RAT	ACH2_DROME		ACH6_HUMAN	ACH3_CHICK	ACHN_CHICK	ACHA_TORMA	ACH4_CHICK	ACHP_HUMAN	ACHN_HUMAN	ACHP_RAT	- 1	ACH3_CARAU			ACH6 RAT	ACH4 DROME	ACHA_RAT	ACHA_MOUSE
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	Length	502	505	505	502	499	498	216	557	503	529	528	267	511	495	499	216	456	494	496	491	461	622	498	205	495	461	512	200	457	493	519	457	457
*	Query	7	46.8	46.6	46.2	45.7	45.1	36.8	36.7	36.0	36.0	36.0	35.9	35.7	35.1	34.9	34.7	34.5	34.4				33.9											33.4
	Score	$^{\circ}$	2	12	1232.5	218	12	980.5	979	960	960	٦,	956.5	an a	936.5	930	ď	918.5	918	•	908.5	906	904	903.5	902.5	902	668	6.888	868	96	896.5	93	890	889
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P26153 gallus gall P49581 gallus gall P19370 carassius a Q9880 brachydanio P43681 homo sapien P05377 xenopus lae P04755 drosophila P45963 caenorhabdi P02708 homo sapien O70174 mus musculu P2708 homo sapien
ACHP_CHICK ACH6_CHICK ACHA_BRARD ACH4_HUMAN ACH2_XENLA ACH3_DROME ACH3_DROME ACH9_CAEEL ACH4_RAT ACH4_RAT ACH4_RAT ACH4_RAT ACH4_RAT
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ALIGNMENTS

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TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCLELLUIAN LOCATION: Integral membrane protein.
SUBCELLUIAN LOCATION: Alpha-7 transcripts transiently accumulate in the developing optic tectum between E5 and E16.
                                                                                                                                                                                                                                                                    FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
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(AY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

L-SA, T: SUPPRESSES INHIBITION BY THE

OPEN CHANNEL BLOCKER QX-222.

QR -> ET (IN REF. 3).
                                                                                        MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC. MEDLINE=93024917; PubMed=1383829; Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S., Changeux J.-P., Bertrand D.; "Mutations in the Channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic."; Nature 359:500-505(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.5%; Score 1267; DB 1; Length 502; 48.6%; Pred. No. 8.9e-99; ive 83; Mismatches 144; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                   bungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572325D4309AD2FD CRC64;
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EXTRACELLULAR
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InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGROOBGO; LIC;
                          nicotinic receptor.";
Nature 353:846-849(1991).
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PDB; 1KC4; 17-APR-02.
PDB; 1KL8; 17-APR-02.
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502 AA;
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                                                                        IDDDFRHPQAQQ 404
MGLRALMIMILAAAGLV-----RESLQGEFQRKLYKELLKNYNPLERPVANDSQPLT 52
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Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
From the SH-SYST cell line and determination of pharmacological
properties of native receptors and functional alpha 7 homomers
expressed in Kenopus oocytes.";
                                                                                                                                                           YGGWSLDLQMQE---ADISGYISNGEWDLVGIPGKRTESFYECCKEPYPDITFIVTMRRR
                                              61 LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV
                                                                                                                                                                                                                                                                                                                TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
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                                                                                                                                    LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                                                                                                                          YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH7_HUMAN STANDARD; PRT; 502 AA.
195544 (D15826, O96RH2; 099555; O9RXH0;
01-UNN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
8-FPB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR NACHRA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 AAMVUDRICLIIFTLFTIIATLAVLLSAPHIM 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Pharmacol. 45:546-554 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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SEQUENCE FROM N.A.
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MEDINE=97162233; PubMed=9009220; Groot Kormelink P.J., Luyten W.H.M.L.; Groot Kormelink P.J., Luyten W.H.M.L.; Groot Kormelink P.J., Luyten W.H.M.L.; actoring and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32."; FEBS Lett. 400:309-314(1997).
                                                                                     Groot Kormelink P.J., Luyten W.H.M.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                    TISSUE=Epidermal keratinocytes;
                                                                                                                                                                                                                        SEQUENCE OF 24-502 FROM N.A.
                                                                                                                                                                                                                                                                        nicotinic receptor subunit
Genomics 19:379-381(1994).
         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                     SPECTROMETRY
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                                                                                                                                                                                                   receptor."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 118-129 FROM N.A.
MEDLINE=21818878; PubMed=11829490;
Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
H. 3-Mb map of a large segmental duplication overlapping the alpha7-
nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
Genomics 79:197-209(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein expression map database.";
Proteomics 2:212-223(2002).
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and chromosomal localization of the human alpha
                                                                                                                                                                                                                                          Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T., Lee J., Tian J., Glordano T., "Cloning and sequence of the human a7 nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A., Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J., "Cluster analysis of an extensive human breast cancer cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
MASS SPECTROMETRY: NW=54157.68; METHOD=MALDI.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane.
SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-bungarotoxin. The structure is probably pentameric (By
Arredondo J., Grando S.A., "Cloning cholinergic receptors in human keratinocytes.", Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subunit gene (CHRNA7).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Breast cancer;
MEDLINE=21829512; PubMed=11840567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94245214; PubMed=8188270;
                                                                                                                                                                                                                                                                                                                                                                                                              Drug Dev. Res. 30:252-256(1993).
                                                                                                                                                               SEQUENCE OF 17-502 FROM N.A.
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EMBL; X70297; CAA49778.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 DVDERNQVLTTNIMLQMSWTDHYLQMNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 APAGLILLICLLWPRGARCGYHEKRLLHHILDHYNVLERPVVNESDPLOLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                                      BY SIMILARITY.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70; Gaps
                                                                                            POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL). (POTENTIAL). (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTE
N-LINKED (GLCNAC. .) (POTE
N-LINKED (GLCNAC. .) (POTE
A -> G (IN REF. 1 AND 7)
S -> N (IN REF. 2 AND 6).
S -> P (IN REF. 2 AND 6).
C -> S (IN REF. 2 AND 6).
RA -> G (IN REF. 8).
RA -> G (IN REF. 8).
RA -> G (IN REF. 8).
W, D94B3A482EAAOB42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                46.8%; Score 1246; DB 1; Length 5 46.0%; Pred. No. 5.2e-97; ive 86; Mismatches 126; Indels
                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                         ALPHA-7 CHAIN.
                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                              POTENTIAL
1; U40583; AAA83561.1; -.
1; U6436; AAB40114.1; -.
1; Y08420; CAA6967.1; -.
1; AZ8355; AAK68111.1; -.
1; L2827; -; NOT ANNOTATED_CDS.
1; Z23141; CAA80672.1; -.
                                                                                                                                                                                                                            fransmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                56449 MW;
                                                    EMBL, AF332758, AAK19515.1;
PIR, G02259, G02259.
PIR, 137185, ACHUA7.
                                                                                HGNC:1960; CHRNA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240; Conservative
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133
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502 AA;
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                                                                               Genew;
                                                                                                                                                                                                                                     SIGNAL
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                          EMBL;
EMBL;
EMBL;
EMBL;
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46 N-
90 N-
133 N-
56631 MW;
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                                                                                                                                                                                                                                                                       Local Similarity 47.1
nes 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
255
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317
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90
133 1
502 AA;
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TISSUE=Brain;
  231
262
296
318
318
470
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                                      TRANSMEM
DOMAIN
                                                                                             DISULFID
                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                        CARBOHYD
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                  TRANSMEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                 392
                                                                                                                        416
                                                                                                                                                            452
                                                                                                                                                                                                   452
                              -VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                     BY SIMILARITY.

NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN.

EXTRACELLULAR (POTENTIAL).
                                                                                                                  361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                            393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 26:399-402 (1995).
-!- FUNCTION. After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-1093 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUE=Brain; MEDLINE=95324936; PubMed=7601470; Orr-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.; "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic_channel; Glycoprotein; Signal;
      MEMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                                                                                                                                                                                                                                                              SEAVCSEWKFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bungarotoxin. The structure is probably pentameric
                                                                                                                                                                                                                                          DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
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                                                                                                                                                                                                                                                                                                                                                                                 502
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PIR, A57175; A57175.
MGD; MGI:99779; Chrna7.
InterPro; IPR006202; Neu channel memb.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan LBD.
Pfam; PF02931; Neur chan LBD.
Pfam; PF02931; Neur chan memb; 1.
PRINTS; PR00252; NRĪCONCHĀNNEL.
                                                                                                                                                                                                     -------GGOPPEG-
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Multigene family.
                                                                                     ------SATTPPPAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L37663; AAC42053.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGROOSEO; LIC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetylcholine receptor.";
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                         -DEHILH
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                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ENGAGLAAHSCFGV------DYELSLILKEIRVITDOMRKDDEDADISR
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MGGRARRSHLAAPAGLILLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MCGRRGGIWLALAAALLHV-----SLQGEFQRRLYKELVKNYNPLERPVANDSQPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ol-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR ACRA7.
Eukattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGE-
                                                                                              POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
                                                                                                                                                                                    (BI SLMILMAKIII).
N-LINKED (GECNAC. . .) (POTENTIAL)
N-LINKED (GECNAC. . .) (POTENTIAL)
N-LINKED (GECNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                 Length 502;
                                                                                                                                                                                                                                                                                                                              ; Score 1241; DB 1; Length 5; Pred. No. 1.4e-96; 90; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                   C9312E5226D120E3 CRC64;
                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
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POTENTIAL
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291 PLJAQYFASTWIIVGLSVVVTVIVLRYHHHDPDGGKMPKWTRIILLNWCAWFLRMKRPGE 350
        54 YFSLSLLQIMDVDEKNQVLTTNIWLQMSWTDHYLQWNMSEYPGVKNVRFPDGQIWKPDIL 113
                                                                                                                                     LYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVABTMPATSDAV 301
                                                                                                                                                                                                                                       399 PTPDSGVVCGRLACSPTHDEHLMHGAHPSDG-DPDLAKILEBVRYIANRNRCQDESEVIC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane.
SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-bungarotoxin. The structure is probably pentameric (By similarity). Homo-oligomer of the short form gives rise to unfunctional channels, as does coexpression of both long and short
                                              :|||||| ||:|: |||: ||||: |||||| 114 INNADABERFDATFHINULVNASGHCQYLPPGIFKSSCYIDVRWFPFDVQQCKLKFGSWSY
                                                                                                351 DKVRPACQHKPRRCSLASVELSAGAGPPTSN------GNLLYI--GFRGLEGMHCA
                                                                                                                                                                                                                                                                                          400 PQAQQPQCCRYYRGGEENGAGL--AAHSCFGVDYELSLILKEIRVITDQMRKDDEDADIS
                                                                                  182 DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKT
                                                                                                                                                                                      PLLGTYFNCIMEMVASSVVST1L1LNYHHRHADTHEMSDW1RCVFLYWLPWVLRMSRPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOId=P54131-2; Sequence=VSP 000075;
TISSUE SPECIFICITY: At least in chromaffin cells.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                          458 RDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                      FROM N.A. (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                    499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P54131-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        forms of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                  BOVIN
                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACH7 BOV
P54131;
                                                                                                                                                                                                                                                                                                                                                                                                        ACH7_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHRNA7
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                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content, is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 SFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN,
                                                                                                                                     similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                          by alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 502;
alpha 7: a nicotinic cation channel highly permeable to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEURONAL ACETYLCHOLINE RECEPTOR ALPHA-7 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                    SUBUNIT: Forms a homo-oligomeric channel blocked by albungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 141; Indels
                                                                                  Bounce o.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00996E74EC7B9A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N -> F (IN RFF ?)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> F (IN REF. 2)
-> R (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1232.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, L31619; AAC33136.1; -...
PIR; T01378; T01378
InterPro; IPR006029; Neu channel memblinterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur chan LBD.
Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan LBD; 1.
PRINTS; PR00222; NEICCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                               STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Multigene family.
SIGNAL 1 22 BY
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                         Neurosci. 13:596-604(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56410 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S53987; AAB25224.2; -.
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                                                  SEQUENCE FROM N.A.
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                                                                                                                 REVISION TO 363
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262
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                                                                             Boulter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                       ACH1 CA
P48180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                           RESULT 6
ACH1_CABEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDD 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 VDEKNQVLTTVIWIMLQMTWTDHYLQWNASEYPGVKTVRFPDGQIWKPDILLYNSADERFDA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 TYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQD 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ADISGYIPNGEWDLVGVLGKRSEKFYECCKEPYPDVTFTVSIRRRTLYYGLNLLIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 VDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006202; Neur_channel memb.
InterPro; IPR006202; Neur_channel memb.
InterPro; IPR006202; Neur_channel.
InterPro; IPR006202; Neur_channel.
Pfam; PF02931; Neur_channemb; 1.
Pfam; PF02932; Neur_channemb; 1.
PRINTS; PR00252; NEUROYR ION CHANNEL, 1.
PROSITE; PS00236; NEUROYRI ION CHANNEL, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Nissing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                          ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.7%; Score 1218.5; DB 1; Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1e-94;
80; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                  ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEE5D0B3820D42D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
BY SIMILAR
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                                                                                                                       EMBL; X93604; CAA63802.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        499 AA;
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228
259
293
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147
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130
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TRANSMEM
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--DPDLAKILEEVRYIAHRFRCQD 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson J., Wohldmann P., Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
- FUNCTION: Possible acetylcholine receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Bristol N2;

BablinEs $9619479 & PubMed=8627624;
Ballivet M., Alliod C., Bertrand S., Bertrand D.;
"Nicotinic acetylcholine receptors in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mormbep; F2566.3; CE09639.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neu_channel_memb.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR00231; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
ITGRFAMS; TIGROGO, LIC; 1.
TIGRFAMS; TIGROGO, LIC; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
                                                                                                          491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA-TYPE CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                     EDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM
                                                                                 CYTOPLASMIC (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                              498 AA
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     --SEG--
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J. Mol. Biol. 258:261-269(1996)
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EMBL; AF022973; AAC25796.1; -.
PIR; S68588; S68588.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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CARBOHYD
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                           NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG 196
                                                                                                                                                                                                            DISSFUTNGEWELIGUPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIA 256
                                                                                                                                                                                                                                                                                                                                                    SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA 316
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WARDLINE-98424077; PubMed=9753155;
WARDLINE-9843155;
WARDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
                                                                                                                                             17 LLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEK
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                                                                                        Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARA1)
93 N-LINKED (GLCNAC. . .) (POȚENTIAL)
57169 MW; E463ABB40AC9FA82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQC-CRYYRGGEENGAGLAA-
                                                        Length 498;
                                                45.1%; Score 1201; DB 1; Length 4 46.0%; Pred. No. 3.1e-93; Live 89; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:| |::|: |||:::
FTIFIIVSTIGIFWSAPYLV 497
                                                                                     Matches 230; Conservative
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93
498 AA;
                                                                    Similarity
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                SEQUENCE
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LDTFSICVTVVVLNVHFRSPQTHTMSPWVRRVFIHVLPRLLVMRRPHYRLDPHRSRFAGL
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Pfam; PF02931; Neur chan memb; 1.
PRINTS; PR00222; NRICONCIANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00336; NEUROTE ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 LLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 VIGAGETILWDEGSPGVPAPPRPPCAPP-----LAPCAAC----APAEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-LIKE CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 NNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILMARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.5%; Pred. No. 1.1e-/%;
tive 75; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 MVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E7A71E8C45D13BD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.8%; Score 980.5; DB 1
40.5%; Pred. No. 1.1e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                           EMBL; Y09795; CAA70928.1; -.
InterPro; IPR006029; Neu channel memb.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur channel.
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132
233
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132
233
516 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S12359; S12359.

InterPro: IPR0060029; Neur_channel memb.

InterPro: IPR006201; Neur_channel.

Pfam; PF02931; Neur_chan LBD.

Pfam; PF02932; Neur_chan memb; 1.

PRINTS; PF02925; NEURCHANNEL.

IIGREAMS; TGR00860; LIC; I.

PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.

Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
                                                                                                                                                                                                                                                                                                MEDLINE=91092263; PubMed=1702381;
Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
Darlison M.G., Sattelle D.B., Barnard B.A.;
Darlison M.G., Sattelle D.B., Barnard B.A.;
Darlison M.G., Sattelle D.B., Barnard B.A.;
Esquence and functional expression of a single alpha subunit of an insect nicotinic acetylcholine receptor.";
EMBO J. 9:4391-4398(1990).

-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .) (POTENTIAL) . .) (POTENTIAL)
                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 41, Last amnotation update)
28-PEB-2003 (Rel. 41, Last amnotation update)
Acetylcholine receptor protein, alpha-Li chain precursor.
Schistocerca gregaria (Desert locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthoptero: Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
NCBI_TaxID=7010;
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N-LINKED (GLCNAC.
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|:|| | |||| :: ::| || || || 487
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                                   4 ALPPMLILILILILILILIHPAAANPDAKRLYDDLLSNYNRLIRPVSNNTDTVLVKKIGLRLSQL
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                                                                                                                                                                                                                                                  131 DSTYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL--
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11 AAPAGLILILICILWPRGARCGYHEKRILLHHILIDHYNVLERPVVNESDPLQLSFGLTLMQI
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"Expression of mRNMs in human thymus coding for the alpha 3 subunit off a neuronal acetylcholine receptor.";
Exp. Neurol. 111:175-180(1991).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDINE=9024526; PubMed=2336208;
FORDARATÍ D., Chini B., Tarroni P., Clementi F.;
"Molecular cloning of human neuronal nicotinic receptor alpha
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MEDLINE=97062879; PubMed=8906617;
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Gaps

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36.7%; Score 979; DB 1; Length 557; 40.0%; Pred. No. 1.6e-74; ive 88; Mismatches 160; Indels '

Conservative

Best Local Similarity Matches 217; Conserv

Query Match

Event=Alternative splicing; Named isoforms=2;

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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Richards S.W., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Allalon D.K., Mumny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Generation and initial analysis of more than 15,000 full-length
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MEDLINE=99118870; PubMed=9921897;
Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.;
"The structures of the human neuronal nicotinic acetylcholine receptor beta2- and alpha3-subunit genes (CHRNB2 and CHRNB3).";
Hum. Genet. 103:645-653(1998).
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Groot Kormelink P.J., Luyten W.H.M.L.;
"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAchR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32.";
FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
MEDLINE=21342809; PubMed=11450844;
Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
"Characterization of the human beta4 nAChR gene and polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Epidermal keratinocytes;
Arredondo J., Grando S.A.;
"Cloning cholinergic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A., Chavez Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.; Chavez Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.; Comparative structure of human neuronal alpha 2-alpha 7 and bacta 4 nicotinic acetylcholine receptor subunits and functional beta 4 subunits."; alpha 3, alpha 4, alpha 7, beta 2, and J. Mol. Neurosci. 7:217-228(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=22388257; PubMed=12477932;
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-!- SUBUNIT: Neuronal AChR seems to be composed of two different type of subunits: alpha and non-alpha (betA).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:

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MWW; 118503; ---

R GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.

BR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.

BR GO; GO:0005215; F:transporter activity; TAS.

BR GO; GO:0005215; F:transporter activity; TAS.

BR GO; GO:0007165; P:signal transduction; TAS.

BR GO; GO:0007165; P:signal transduction; TAS.

BR GO; GO:0007165; P:signal transport; TAS.

BR GO; GO:0007165; P:signal transport; TAS.

BR GO; GO:0006210; P:transporter activity; TAS.

BR InterPro; IPRO06202; Neur_chan.elb.

BR InterPro; IPRO06202; Neur_chan.elb.

BR FRINTS; PRO0223; Neur_chan.emb; 1.

BR PRINTS; PRO0223; Neur_chan.emb; 1.

BR RINTS; PRO0225; NEUROTE ION CHANNEL; 1.

BR ROSITE; PS00236; NEUROTE ION CHANNEL; 1.

R RCCEPLOT; POSISSHING: MEMBARD; Indic channel; Glycoprotein; Signal; XW Receptor; Postsynaptic membrane; Indigene family; Alternative splicing; Polymorphism.

FT SIGNAL

SIGNAL

PROFERED PROFEIN,
                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                     Note=No experimental confirmation available, SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSLPIALSP -> ALAAPGAVA (IN REF. 2).

LSPP -> CRA (IN REF. 1).

D -> G (IN REF. 1).

I -> S (IN REF. 1).
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
MALAV -> MGSGPL (in isoform 2).
/FTIde_VSP_000073.
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                       IsoId=P32297-2; Sequence=VSP 000073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
               Name=1;
IsoId=P32297-1; Sequence=Displayed;
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EMBL; AJ007783; CAA07682.1; --
EMBL; AJ007784; CAA07682.1; JOINED.
EMBL; AJ007785; CAA07682.1; JOINED.
EMBL; AJ007785; CAA07682.1; JOINED.
EMBL; AJ007787; CAA07682.1; JOINED.
EMBL; BC001642; AH01642.1; --
EMBL; BC002996; AAH01642.1; --
EMBL; AF385584; AAK68110.1; --
EMBL; AF385584; AAK68110.1; --
EMBL; A53956; A53956.
                                                                                                                                                                                                                               EMBL; M86383; AAC84176.1; -.
EMBL; M37981; AAA59942.1; -.
                                                                                                                                                                                                                                                             U62432; AAB40110.1; -.
Y08418; CAA69695.1; -.
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                                                                                                                                                                                                                                                                                                             STYPTNVVVRNNGSCLYVPPG1FKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
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                                                                                                                                                                       SPPRILILILISLIP-VARASEAEHRLFERLFEDYNEIIRPVANVSDPVIIHFEVSMSQLV 70
                                                                                                                                             12 APAGLILLICLINPRGARCGYHEKRILHHILDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                               DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q15822; Q9HAQ3;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
CHRNA2.
                                                                                                      30;
                                                            Length 503;
                                                        36.0%; Score 960; DB 1; Length 50 ilarity 41.0%; Pred. No. 5.6e-73; Conservative 90; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM M.A.
Groot Kormelink P.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
L -> V (IN REF. 1).
     8A9EBC5D71AEC7D6 CRC64;
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MEDLINE=97062879; PubMed=8906617;
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Neurosci. 7:217-228(1996)
                                                                                                   106
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Mammalia; Butheria; Primates;
                   57309 MW;
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  430
503 AA;
                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .; TAS.
                                                                                                                                                                                                                                                           SUBUNIT: Neuronal AChR seems to be composed of two different types of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be combined to beta-2 or beta-4 to give rise to functional receptors. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RARRSHLAAPAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSF
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R Genew; HGNC:1956; CHRNA2.

R MIM; 118502; -

R QG: QG: CORS92; CINICOTINIC acetylcholine-gated receptor-chan. ..;

GO; QG: CORS92; CINICOTINIC acetylcholine-gated receptor-chan. ..;

GO; GO: OOU1564; F: acetylcholine receptor activity; TAS.

GO; GO: OOU165; P: signal transduction; TAS.

R GO; GO: COROT165; P: signal transduction; TAS.

InterPro; IPRO06602; Neur channell memb.

InterPro; IPRO06602; Neur chan LBD.

InterPro; IPRO06201; Neur chan LBD.

R Ffam; PFC0293; Neur chan LBD.

R Pfam; PFC0293; Neur chan LBD.

R Pfam; PFC0293; Neur chan LBD.

R Pfam; PFC0293; Neur chan LBD;

R PGC0293; Neur chan LBD;

R PGC0394; Neur chan LBD;

R PGC0395; N
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BY SIMILARITY.

ASSOCIATED WITH RECEPTOR ACTIVATION

(BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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EMBL, Y16281, CAA76154.1; -.
EMBL, AF311103; -, NOT_ANNOTATED_CDS.
Genew, HGNC:1956; CHRNA2.
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                                                                                                                                                                                                                                                            TINLIIPCLLISCLTVLVFYLPSDCGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPL 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 HIASGASGPKAEALLQEGE---LILSPH------MOKALEGVHYIADHLRSEDADSSV 489
149 NNADGEFAVTHMTKAHLFSTGTVHWVPPAIYKSSCSIDVTFFPFDQQNCKMKFGSWTYDK 208
                                                                       184 YQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLY 243
                                                                                                                                                                                                                       YFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 303
                                                                                                                                                                                                                                                                                                                                                                  LGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSAT 363
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                                                                                                                                       209 AKIDLE-OMEQTVDLKDYWESGEWAIVNATGTYNSKKYDCCAEIYPDVTYAFVIRRLPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                      328 IGEYLLFTMIFVTLSIVITVFVLNVHHRSPSTHTMPHWVRGALLGCVPRWLLMNRP----
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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"Genes expressed in the brain define three distinct neuronal
nicotinic acetylcholine receptors.";
BMBO J. 7:555-601(1988).
-!- FUNCTION: After binding acetylcholine, the AChR responds by an
extensive change in conformation that affects all subunits and
lads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane.

-!- SUBUNIT: Neuronal AChR seems to be composed of two different type of subunits: alpha and non-alpha (also called beta). A functional receptors seems to consist of two alpha-chains and three non-alpha chains.
-!- SUBCELIULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 TPPPARVPPPDLELRERSSKSLLANVLD-----IDDDFR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 SRDWKFAAMVVDRLCLIIFTLFTIIATLAVLL 488
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EMBL, X07340; CAB59645.1; JOINED.
EMBL, X07341; CAB59645.1; JOINED.
EMBL, X07342; CAB59645.1; JOINED.
EMBL, X07344; CAB59645.1; JOINED.
EMBL, X07344; CAB59645.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
                                                                                                                                                                                                                                                                     NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN. EXTRACELLULAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 RSPSTHTMPHWVRSFFLGFIPRWLFMKR-----PPLLLPAEGTTGQYDPPGTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
            PIR, S00377; ACCH2N.

R InterPro; IPR006029; Neu_channel_memb.

R InterPro; IPR006202; Neur_chan_LBD.

R InterPro; IPR006202; Neur_chan_LBD.

R Pfam; PF02931; Neur_chan_memb; 1.

R Pfam; PF02932; Neur_chan memb; 1.

R PRINTS; PR00252; NRIONCHĀNNEL.

R TIGRRĀMS; TIGRROWS60; LIC; 1.

PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.

R POSITE; PS00236; NEUROTR_ION_CHANNEL; 1.

R POSITE; PS00236; NEUROTR_ION_CHANNEL; 1.

R PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.

R PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E76C6360AF876364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 959; DB 1;
Pred. No. 7.2e-73;
                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKSLLANVLDIDDDFRHPQAQQPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMVVDRLCLIIFTLFTIIATLAVLL 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60675 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.0%;
39.2%;
AJ250360; CAB59625.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.21
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  520
410
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223
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104
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567

PRT;

STANDARD;

ACH1_DROME ID ACH1_DROME

RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                              RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ranatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George B.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George B.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Render R.G., Handell M.D., Zhang Q., Chen L.X., Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Freiffer B.D., RA Ballew R.M. Basu A., Baxendala J., Bayaktaroglu L., Beasley E.M., Beson K.Y. Benco P.V., Barman B.P., Bhandari D., Bolshakov S., Buttis R.C., Busam D.A., Eutler H., Cadieu E., Center A., Chandra I., Rakeva D., Botchan M.R., Bouck J., Exchetein P., Botchiar I., Raber B.D., Buttis R.C., Busam D.A., Lauler H., Cadieu E., Center A., Chandra I., Raberis R.C., Busam D.A., Lauler H., Cadieu E., Center A., Chandra I., Raberis R.D., Deucher A., Deng C., May A.D., Davies P., And Chandra I., Chandri R.A., Cong F. Gorrell J.H., Gu Z., Gunn P., Botchan M., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Botchan K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Botchan M., Harvey D.A., Heinam T.J., Wei M.-H., Ibegwan C., Jalail M., Kalush F., Karpen G.H., Wei M.-H., Ibegwan C., Jalail M., Kalush F., Karpen G.H., Wei M.-H., Ibegwan C., Jalail M., Kalush F., Karpen G.H., Wei M.-H., Ibegwan D., Merkulov G., Milshina M.V., Mobarry C., Morris J., Moshrefi A., Month G.M., Pittman G.S., Pan S., Pollard J., Puri, J., Li Z., Liang Y., Lin X., Allanct E., Morluck R.A., Nixon K., Nusskern D.M., Palazollo M., Pittman G.S., Pan S., Pollard J., Puri, V., Reanigon M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun B., Spine H., Wei S., Shen H., Wang C., Stapleton M., Strong R., Sun S., Shen H., Wang C., Yen B., Woother E., Wang G., Yen C., Stapleton M., Strong R., Sun S., Shen H., Wang C., Yen R., Woother S., Wang C., Stapleton M., Stung G., Shen H., Wang C., Yen R., Nelson M., Walliams S.M., Woodage T., Woother S., Wang C., Stapleton M., Stung G., Shen H., Wang C., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Bernan B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
                                                                                                                                                                                                                                 MEDLINE=88283626; PubMed=2840281;
Bossy B., Ballivet M., Spierer P.;
"Conservation of neural nicotinic acetylcholine receptors from brosophila to vertebrate central nervous systems.";
EMBO J. 7:611-618(1988).
                                                                                                            Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
P09478; Q9VC74;
01-MAR-1989 (Rel. 10, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 1 precursor.
NACR-ALPHA-96AA OR ACRB OR ALS OR ACR96AA OR CG5610.
                                                                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LLLCILMPRGARCGYHEKRILHHILDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKN 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 VVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL----QLQD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---EGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family; Polymorphism.
                                                                                                                                       TISSUE SPECIFICITY: CNS in embryos. DEVELOPMENTAL STAGE: Late embryonic, late pupal and second instar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                      leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
                     FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and
                                                                                                                                                                                                           SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.9%; Score 956.5; DB 1; Length 567; 38.2%; Pred. No. 1.3e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08E1F721FB2A92AC CRC64;
                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y -> H.
L -> H (IN REF. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006029; Neu Channel memb.
InterPro; IPR006029; Neur Chan LBD.
InterPro; IPR006202; Neur Channel.
Pfam; PF02931; Neur Chan LBD; 1.
Pfam; PF02932; Neur Chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
TIGRPĀNS; TIGR0860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0000036; nAcR-alpha-96Aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X07194; CAA30172.1; -.
EMBL; AE003747; AAF56301.2; -.
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2290
325
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532
163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S00381; ACFFA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                        larvae stages.
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272
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TRANSMEM
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InterPro; IPR006202; Neur_chan_LBD
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                                                                                                                                                                                                                                                                                           56
106
212
494
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266
292
329
329
484
402
402
174
225
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106
212
494
511 AA;
                                                                                                          Transmembrane;
SIGNAL
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Q07263;
                                                                                                                                                                        TRANSMEM
TRANSMEM
TRANSMEM
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                                        387
                                                                                            IPCVGISFLSVLVFYLPSDSGEKISLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLL 308
                         CIMEMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPAR 369
                                                                                                                              388 ANVLDI----DDDFRHPQAQ-----QPQCCRYYRGGEENGAGLAAHS-----CFGVDY--ELS 434
                                                                                                                                                                                     493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Neuronal AChR seems to be composed of two different types of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be combined to beta-2 or beta-4 to give rise to functional receptors. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                        427 PSSLPLPGADDDLFSPSGLNGDISPGCC-----PAAAAAAAADLSPTFEKPYAREME
                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                LILKEIRVITDOMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boulter J., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 36, Last sequence update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley, TISSUE-Brain, MEDLINE-88178113; PubMed=2832952; MADLINE-88178113; PubMed=2832952; Mada K., Ballivet M., Boulter J., Connolly J.G., Wada E., Deneris E.S., Swanson L.W., Heinemann S.F., Patrick J.; "Functional expression of a new pharmacological subtype of brain nicotinic acetylcholine receptor.";
                                                                                                                                                                                                                                                                            511 AA
                                                                            VPP-----PPDLE-LRERSSKSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A40110; A40110.
InterPro; IPR006029; Neu_channel_memb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L10077; AAB60900.1; -
EMBL; M20297; AAA40664.1; -
EMBL; M20292; AAA40664.1; JOINED.
EMBL; M20294; AAA40664.1; JOINED.
EMBL; M20294; AAA40664.1; JOINED.
EMBL; M20296; AAA40664.1; JOINED.
EMBL; M20296; AAA40664.1; JOINED.
                                                                                                                                                                                                                                                                                     P12389; 008952;
01-007-1989 (Rel. 12, Created)
15-UUL-1998 (Rel. 36, Last ann
28-FBB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 240:330-334(1988)
                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane.
                                                                                                                                                                                                                                                          370
                         310
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REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| |: :|| || || :|| || 317 TLSIVITVFVLNVHHRSPSTHNMPNWVRVALLGRVPRWLMMNRP-----LPPWELHGSPD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 LKL--SPSYHWLETNMDAGEREETEBEEEE-----DENICVCAGL-PDSSMGVLYG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 ASMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 ASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: | | :: | | : : | | : | | 421 HGGLHLRAMEPETKTPSQASEILLSPQIQKALEGVHYIADRLRSEDADSSVKEDWKYVAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 VDLKDYWESGEWALINATGTYNSKKYDCCAEIYPDVTYYFVIRRLPLFYTINLIIPCLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ELSLILKEIRVITDOMRKDDEDADISRDWKFAAM
                                                                                                                                                                                                                               NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEEN---GAGLAAHSCFGVDY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan lbb; 1.
Pfam; PF02932; Neur_chan memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TRGRAPM; TIGRORG, LIC; I.
PROSITE; PS00256; NBTORGE; NOTHANNEL; 1.
PROSITE; PR00576; NBTORGE; ION CHANNEL; 1.
PROSITE; PR00546; NBTORGE; ION CHANNEL; 1.
PROSITE; PR00546; NBTORGE; IONIC Channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> S (IN REF. 1; AAA40664).
3824E83BB01D613B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 951; DB 1;
Pred. No. 3.3e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
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POTENTIAL.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
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406 SANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVI 465
                                             116 NAVGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWSYDKA 175
                                                                                                                                                                                                                         GTYFNCIMFWVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----G 360
                                                                                                                                                                                                                                              SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQC--CRYYRGGEEN- 417
                                                                                                                                                                                                                                                                                                                            355 NIORPRPFYSAELSNINCFSRIESKVCKEGYPCODGL-----CGYCHHRRAKISNF 405
                                                                                                                                                                                                                                                                                                                                                              418 GAGLA-AHSCFGVDYELSL-----ILKEIRVITDQMRKDDEDADISRDWKFAAMVV 467
                                                                                                        245 FENLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88041184; PubMed=2444984;
Boulter J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann S.F.,
Parrick J.;
              SADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGY
                                                                                 QLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of an acetylcholine receptor alpha 3 gene promoter and its activation by the POU domain factor SCIP/Tst-1.";
J. Biol. Chem. 269:10252-10264(1994).
-:- FUNCTION. After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholine receptor alpha-subunit.";
Nature 319:368-374(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional expression of two neuronal nicotinic acetylcholine receptors from cDNA clones identifies a gene family."; Proc. Natl. Acad. Sci. U.S.A. 84:7763-7767(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-86118671; PubMed=3753746;
Boulter J., Frans K., Goldman D.J., Martin G., Treco D., Heinemann S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang X., McDonough J., Fyodorov D., Morris M., Wang F., Deneris E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   468 DRLCLIFTLFTIIATLAVLL 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHRNA3 OR ACRA3
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                  125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 LTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYN 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006203; Neu channel memb.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur chan LBD.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan memb; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
PROSTRE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                  composed of two different type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                        MEDLINE=92119195; PubMed=1620271; Criado M., Alamo L., Navarro A.; Criado M., Alamo L., Navarro A.; Criado M., Alamo L., Navarro A.; Alamo L., Navarro A.; Alamo L., Navarro A.; Alamo L., Navarro A.; Neurochen receptor from bovine adrenal chromaffin cells."; Neurochem. Res. 17:281-287(1992).
-!- FUNCTION: After binding accepylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Neuronal AChR seems to be composed of two different to subunits: alpha and non-alpha (betA).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BI SIMILMANIII).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 936.5; DB 1; Length 495;
Pred. No. 5.2e-71;
9; Mismatches 181; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPHA-3 CHAIN.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ransmembrane, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89;
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Matches 198; Conservative
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                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
162
195 AA;
                                                                                                                                                       NCBI_TaxID=9913;
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231
263
296
319
468
149
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                                                                                                                                                                                                                                                                                                                                                    membrane.
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CARBOHYD
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALPHA AND NON-ALPHA, BETA, ALPHA-3 SUBUNIT CAN BE COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X03440; CAA21170.1; --
EMBL; M04961; AAA41673.1; --
EMBL; U04961; AAA41601.1; --
INTERPYC; IPRO06202; Neur_chan_LBD.
INTERPYC; IPRO06202; Neur_chan_LBD.
INTERPYC; IPRO06201; Neur_channel.
Ffam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PRO05221; NRUNCHANNEL.
INTERPANS; TICRO0860; LIC; I.
PROSITE; PS000236; NEUROTR ION_CHANNEL; 1.
PROSITE; PS000236; NEUROTR ION_CHANNEL; 1.
PROSITE; PS000236; NEUROTR ION_CHANNEL; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-3 CHAIN.
EXTRACELLULAR.
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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (PROBABLE).

D66C491E832B9C34 (RC64;
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166 N-
56997 MW;
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Db 364 RTFYGAELSNINCFSRADSKSCKEG------YP-CQDGTCGYCHHRRVKISNFSANL 413

Qy 422 ------AAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLC 471

Db 414 TRSSSSESVNAVLSLSALSPEIKEAIQSVKYIAENMKAQNVAKEIQDDWKYVAMVIDRIF 473

Qy 472 LIIFTLFTIATLAVLL 488
```

Db 474 LWVFILVCILGTAGLFL 490

Search completed: May 7, 2004, 11:36:32 Job time : 10.2632 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 11:30:03 ; Search time 31.1579 Seconds (without alignments) 5022.709 Million cell updates/sec May Run on:

US-09-303-232-4

2665 Perfect score:

1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHIMVS 496 BLOSUM62 Scoring table: Sequence:

1017041 segs, 315518202 residues Searched:

Gapop 10.0 , Gapext 0.5

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL 25:* Database :

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_organelle:*
sp_organelle:* unclassified:* sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* rodent:* sp_archeap: sp_plant:* sp_virus:* 10: 11: 12: 12: 12: 14: 17: 17:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

SUMMARIES

QBL,...
QBGmn7 drosup.
Q9vwi9 drosophila
Q9xzi4 heliothis v
~~~752 drosophila Q8t7s2 drosophila Q8t7s1 drosophila Q8t7s1 drosophila Q8t7s3 drosophila Q8t7s0 drosophila Q8t7s9 drosophila Q9v179 drosophila Q9v179 drosophila Q9xzi3 heliothis v drosophila drosophila Description Q8t7v5 Q8T7V5 Q86MN7 Q9VWI9 Q9XZ14 Q8T7S2 Q8T7S1 Q86MN8 Q8T7S3 Q8T7S0 Q8T7R9 Q9XZI3 Query Match Length DB 501 494 494 494 100.0 67.3 67.4 67. 2665 2064.5 2047 2046.5 1803.5 1792.5 1792.5 1791.5 1791.5 Score Result

Q800c7 brachydanio Q7t2u0 fugu rubrip Q9vjt9 drosophila

Q800C7 Q7T2U0 Q9VJT9

13

55.7 51.4 47.7 46.9

1484.5 1371 1272.5 1253 1251

Q8IPE2

494 509

9.99

67.2

| Ogjhd6 mus musculu QTC280 fugur rubrip Q86622 macaca mula Q03481 gallus gall QTC29 fugu rubrip QTC29 fugu rubrip QTC29 fugu rubrip QTC20 fugu rubrip QTC20 fugu rubrip QTC20 fugu rubrip Q91197 caenorhabdi Q8032 caenorhabdi Q81932 caenorhabdi Q1855 caenorhabdi Q1855 caenorhabdi Q1855 caenorhabdi Q8091 mellif Q86077 homo sapien Q8009 aplysia cal Q8009 aplysia cal Q8009 aplysia cal Q915 go oglysia cal Q915 mus musculu Q9611 heliothis v Q8146 mus musculu Q8613 locusta mig Q8149 mus musculu Q8149 mus musculu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | S AA.  S AA.  To update)  To update)  To alpha 7-1 subunit.  St ancth).  In Secta; Pterygota;  Insecta; Ditrysia; Noctuoidea;  Lossata; Ditrysia; Noctuoidea;  Lossata; Ditrysia; Noctuoidea;  Lobus adabases.  ANE PROTEIN (BY SIMILARITY).  TED.  TEA.  IEA.  IEA.  IEA.  IEA.  IEA.  IEA.  IEA.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | mbiane; receptor; |
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| 11 Q9JHD6<br>6 Q866A2<br>13 Q03481<br>13 Q03481<br>13 Q71219<br>13 Q71219<br>13 Q71219<br>13 Q71219<br>13 Q71219<br>5 Q8RD1<br>5 Q8RD1<br>5 Q8RURO<br>6 Q8G133<br>5 Q8RURO<br>5 Q8RURO<br>7 Q8G133<br>5 Q8RURO<br>5 Q8RURO<br>7 Q8G133<br>6 Q8RURO<br>7 Q8G134<br>7 Q8G134                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | PRT; 496 AAA, created) Last sequence u last sequence u last amotation colone, last amotation colone, last sequence u id moth) (Owlet module receptor a liothis.  Inchis. Subunits liothis.  Inchis. Subunits alpha 7 subunits cetylcholine receptor e EMBL/GenBank/DDI NTEGRAL MEMBRANE THE LIGAND-GATED INTEGRAL MEMBRANE INTERIGAND-GATED into membrane; IEA.  THE LIGAND-GATED into membrane; IEA.  THE LIGAND-GATED into membrane; IEA.  THE LIGAND-GATED into membrane into | oscaymapere       |
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| 17 1242<br>19 1239.5<br>19 1239.5<br>20 1219.5<br>22 1166.5<br>23 1150.5<br>24 11141<br>25 1166.5<br>26 1066.5<br>30 994<br>31 975.5<br>31 960<br>32 961<br>34 960<br>35 961<br>36 940.5<br>41 928<br>44 928                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | RESULT 1  Q9XZI3 AC Q9XZI3 DI Q9XZI3; DT 01-NOV-1999 (TERMED DT 01-NOV-1999 (TERMED DT 01-UN-209) (TERMED DT 0 | Transmembrane     |
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SSVVSTILILLNYHHRNADTHEMSEWIRIVFLCWLPWILRMSRPG---RPLILEFPTTPCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
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R GO; GO:0005216; F:ion channel activity; IEA.
R GO; GO:0005216; F:neurotransmitter receptor activity; IEA.
R GO; GO:0006811; P:ion transport; IEA.
GO; GO:0007266; P:synappic transmission; IEA.
R InterPro; IPR006201; Neur_channel.
R InterPro; IPR006202; Neur_channel.
R InterPro; IPR006029; Neur_chan_LBD.
InterPro; IPR006029; Neur_chan_LBD.
R Pfam; PF02931; Neur_chan_LBD; 1.
R Pfam; PF02932; Neur_chan_memb; 1.
R PRIMTS; PR00225; NETONCHANNEL.
R TIGRFAMS; TIGRO0860; LIC; 1.
R PROSITE; PS00226; NERCOTR ION_CHANNEL; 1.
R PROSITE; PS00226; NERCOTR ION_CHANNEL; 1.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor subunit Dalpha7 precursor.
NACRALPA-18C.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                        77.5%; Score 2064.5; DB 5; Length 76.7%; Pred. No. 6.2e-192; ive 32; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                            807 AA; 91223 MW; C8B4F6B34287C8C8 CRC64;
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SEQUENCE FROM N.A.
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REDLINE=21969411; PubMed=11973307; Sattelle D.B.;

MEDLINE=21969411; PubMed=11973307; Sattelle D.B.;

MEDLINE=21969411; PubMed=11973307; Sattelle D.B.;

MEDLINE=21969411; PubMed=11973307;

Talpha6, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a not Highly Conserved Target of Adenosine Deaminase Acting on RNA-Nediated A-to-1 Pre-mRNA Editing."; Genetics 160:1519-1533 (2002).

Mediated A-to-1 Pre-mRNA Editing."; Genetics 160:1519-1533 (2002).

--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

ENBL: AR272778; AAMILY.

ENBL: APPRASE; FEGNO28875; nAcR-alpha-34E.

BR GO: GO:0016021; C:integral to membrane; IEA.

GO: GO:0016021; C:integral to membrane; IEA.

GO: GO: 005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                 LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAAHSCEGUDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTI
                                                                                                              Gaps
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Ol-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 24, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 24, Last sequence update)
Nicotinic acetylcholine receptor Dalpha5 subunit.
NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 (CG4498 OR CG1684) OR CG32975.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bophydroidea; Drosophilaidae; Drosophila.
                                                                                                            ö
                                                            Length 496;
                                                                                                            Indels
          8032FED8515A6210 CRC64;
                                                          Score 2665; DB 5;
Pred. No. 9.4e-251;
                                                                                                            ;
0
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                                                                                                            0; Mismatches
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          56347 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 IATLAVLLSAPHIMVS 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IATLAVLLSAPHIMVS 496
                                                            100.08;
                                                                                 ilarity 100.0%;
Conservative
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             AA;
                                                                                    Similarity
             496
                                                                                    Best Local Sim
Matches 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
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          SEQUENCE
                                                            Query Match
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                                                                                                                                                                                                                                                                                                                         PLIGITY FUCIMEMVASS VVSTILILUYHHRHADTHEMSDWIRCVFLYWL PWVLRMSRPGS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 ATTPPPARVPPP-----HPQA- 402
                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 V----GYECPPPPSSSSSSSSSSKQQIQNVĖLKERŠSKŠLLANVLDIDDDFRCNHRCAS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LAAHSCF--GVDYELSLILKEI 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGRARRSHLAAPAGLILILICLLMPRGARCGYHEKRLIHHILIDHYNVLERPVVNESDPLQL
                                                                                                                                                                                                                                                                                                                                                  DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKT
                                                                                                                                                                                                                                                                                                                                                            16 GGRM----LVVGLGLLIMI-----PACAAGPHEKRLLHALLDNYNSLERPVVNSSDPLQL
                                                                                                                                                                                                                                                                                                                                                                                        LYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV
                                                                                                                                                               NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          496
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 RVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
A Millar N.S.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL. AJ554210; CAD66936.1;
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0015230; F:extracellular ligand-gated ion channel acti
R GO; GO:00190594; F:neurotransmitter receptor activity; IEA.
R GO; GO:00190594; F:neurotransmitter receptor activity; IEA.
R GO; GO:00190594; F:neurotransmitter receptor activity; IEA.
R InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR Fiam; PR02931; Neur_chan_LBD.
DR Pfam; PR02931; Neur_chan_LBD; 1.
DR PRINTS; RR00252; NRIONCHANNEL.
DR PRINTS; RR00252; NRIONCHANNEL.
DR TIGRRAMS; TIGR00860; LIC; 1.
DR PROSITE; P.ELLER.
PROSITE; P.ELLER.
                                                                                                                                                                                                    Length 542;
                                                                                                                                                                                                                      47; Indels
                                                                                                                                                                                 69D2C39746BB74D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0X7-2000 (TrEMBLrel. 13, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                  76.8%; Score 2047; DB 5; 74.4%; Pred. No. 1.8e-190;
                                                                                                                                                                                                                  Matches 399; Conservative 36; Mismatches
                                                                                                                                                                        DALPHA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QQPQCCR-YYRGGEENGAG-
                                                                                                                                                                                542 AA; 60988 MW;
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                                                                                                                                                      35
542
                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                               122
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                                                                                                                                                                                                                                                                                                                                                                                                                          302
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                                                                                                                                                                               SEQUENCE
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CG32538 protein.
NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.
Drosophila melanogaster (Fruit fly).

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RA MEDITME-20196006; Pubbed-1073132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburnen M., Henderson S.N.,

RA Beradon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Barzkataroglu L., Basaley E.M.,

RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Barokatein P., Bolshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Barokatein P., Botshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Barokatein P., Botshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Barokatein P., Botshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Barokatein P., Botsier S.,

RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.,

RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferraz C., Busen D.,

RA Goson K., Doug L.B., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P.,

RA Horbin K.J., Evangelista C.C., Ferraz C., Ferrac S., Pulkov J.,

RA Horbin K.J., Harvey D., Heiman T.J., Harniandez J.R., Harris M..,

RA Hostin D., Houston K.A., Heiman T.J., Harris M.,

RA Hostin D., Houston K.A., Heiman T.J., Harris M.,

Allu K., Malush F., Karpen G.H., Ke Z., Kemniscon J.A., Ketchum K.A.,

RA Hostin D., Houston K.A., Liu J., Li Z., Liang Y., Lin X.,

Allu K., Mattel B., Moline B. Murphy L., Muzny D.M., Nelson D.I.,

RA Merkulov G., Milshina M.V., Mobarry C., Morits J., McShrefi A.,

Rount S.M., Moly M., Murphy B., Murphy D., Waissern D., Moshrefi A.,

Rander K., Remington K., Saudes M., Strong R., Suith T.,

Shien B.C., Siden-Kiamos I., Simpson M., Strong R., Suith T.,

Rander R., Molom K.A., Nixon K., Wu D., Yang S., Yao Q.A.,

Randiams S.M., Woodaer T., Wone, Wang S., Yao Q.A.,

Randiams S.M., Woodaege T., Wonley W., Sung S., Hang C., Siden-Kiamos I., Simpson M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Bussan D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Photanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., "Sequencing of Drosophila melanogaster genome.";
"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       STRAIN=Berkeley;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 GPHEKRLLHALLDNYNSLERPVVNESDPLOLSFGLTLMQIIDVDEKNOLLITNIWLKLEW
                                                                                                                                                                                                                                                                                                                                                                      NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                           99 NDMNLRWNSSEFGGVRDLRIPPHRLWKPDVLMYNSADEGFDGTYATNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVPGKRNEIYYNCCPEPYIDITFAILIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKLSLGVIIILSLIVFINMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILIINYHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LAAHSCF--GVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDR
                                                                                                                                                                                                                                                                                                                                                                                                                   PGIFKSTCKIDITWFFFDDORCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
                                                                                                                                                                                                                                                                                                                         GYHEKRILHHILDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIELRERSSKSLLANVLDIDDFR--HPQA----QQPQCCR-YYRGGEENGAG-
                     Venter C.J.;
                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                            545;
                                                                           Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
REMBL; AE003511; AAF48950.2; --
REMBL; AE003511; AAF48950.2; --
REMBL; AE0001020] C::membrane; IEA.
GO; GO:0005230; F::extracellular ligand-gated ion channel aci
GO; GO:0005230; Neur channel.
R InterPro; IPR06620; Neur channel.
R Pfam; PF02931; Neur chan LBD.
R Pfam; PF02932; Neur chan LBD; 1.
R PRINTS; PR00252; NRIONCHĀNNEL.
TIGRPOMS; TIGROOMGGO; LIC; 1.
R PROSITE; PS00236; NEURORR ION CHANNEL; 1.
R SEQUENCE 545 AA; 61517 MW; 7B83025107A66209 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPPARVPPPP----
                                                                                                                                                                                                                                                                            5; Length
                                                                                                                                        receptor activity; IEA
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                            channel
                     S.E., Gibbs R.A., Rubin G.M., Vente
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                            76.8%; Score 2046.5; DB 5; 77.7%; Pred. No. 2.1e-190; ive 32; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCLIIFTLFTIIATLAVLLSAPHIMVS 496
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                        Adams M.D., Celniker
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 394; Conserv
             FROM N.A.
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219
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OSXZI4; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-UIM-2003 (TrEMBLrel. 24, Last annotation update) Putative nicotinic acetylcholine receptor alpha 7-2 subunit.

Q9XZI4

BHHH

Q9XZI4

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                                                                                                                                                SEQUENCE FROM N. Adamczewski M.;
SEQUENCE FROM N. Adamczewski M.;
Schulter T., Oellers N., Adamczewski M.;
"Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha? subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

C. -- SUBCELDULAR LOCATION: INTEGRAL MEMBRANB PROTEIN (BY SIMILARITY).

EMBL, AF143847; AAD32698.1; --
RM GO, GO:0016021; C.:Integral to membrane; IEA.

RM GO, GO:0016021; C.:Integral to membrane; IEA.

RM GO; GO:001621; F:ion channel activity; IEA.

RM GO; GO:0005216; F:ion channel activity; IEA.

RM GO; GO:0005216; F:ion transport; IEA.

RM GO; GO:0005216; P:synaptic transmission; IEA.

RM GO; GO:0005219; Neur_chan.BD.

RITGETPO; IPR006202; Neur_chan.BD.

RITGETPO; IPR006202; Neur_chan.BD.

RM Fam; PF02931; Neur_chan.BD.

RM PERNINS; PR00252; Neur_chan memb; 1.

RM PRINTS; PR00252; NRICHANNEL.
                                                                                                                                                                                                                                                                                                                                                              .; IEA
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              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis
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68.7%; Pred. No. 8.9e-167;
ive 53; Mismatches 78;
(Owlet moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLIIFTLFTIIATLAVLLSAPHIMV 495
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(Noctuid moth)
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Best Local Similarity 68.7<sup>3</sup>
Matches 347; Conservative
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                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21969411; PubMed=11973307; Grauso M., Reenan R.A., Culetco E., Sattelle D.B.; Grauso M., Reenan R.A., Culetco E., Sattelle D.B.; Subvist Benes, Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-1 Fre-mRNA Editing."; Genetics 160:1519-1533 (2002).

-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-: SUBLIARINIARIES BELOGATION THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SPLPASLSLFVLLIFLAIIKESCQGPHEKRLINHLLSTYNTLERPVANESEPLEVKFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 SHLAAPAGLLILLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
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R FlyBase; FBGN0032151; nAcR-alpha-30D.
R GO; GO:0016621; clintegral to membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti...;
R GO; GO:0005246; F:ion channel activity; IEA.
GO; GO:0005246; F:ion channel activity; IEA.
GO; GO:000524; F:ion transport; IEA.
R GO; GO:0006811; P:ion transport; IEA.
R GO; GO:0006811; P:ion transport; IEA.
R GO; GO:000268; P:synaptic transmission; IEA.
R InterPro; IPR006201; Neur_channel.
R InterPro; IPR006202; Neur_channel.
R InterPro; IPR006202; Neur_channel.
R Ffam; PF02931; Neur_channel.
                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type II.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00236; NEUROTR ION CHANNEL; 1. Glycoprotein; Ionic channel; Fostsynaptic membrane; Receptor;
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                                                       494 AA.
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TIGRFAMS; TIGR00860; LIC; 1.
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Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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RESULT 6
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                           367 PARVP-PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAA--
                                                                                                   HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21969411; PubMed=11973307;
Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Grauso M., Recordinic Acetylcholine Receptor Subunit Genes,
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-LO-I Pre-mRNA Editing.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARI:
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
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Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot Neoptera; Endertygota; Diptera; Bidopterygota; Diptera; Brachycerygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR006029; Neu channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan memb; 1.
PRINTS; PR00252; NRĪONCHĀNNEL.
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472 VFTLFTIIATVTVLLSAPHIIV 493
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MEDLINE=19969411; PubMed=11973307;
MEDLINE=21969411; PubMed=11973307;
MEDLINE=21969411; PubMed=11973307;
A Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Arauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Arauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Twovel Putrative Nicotinic Acetylcholine Receptor Subunit Genes,
The Color of Pre-mRNA Editing.";
Mediated A-to-1 Pre-mRNA Editing.";
Mediated A-to-1 Pre-mRNA Editing.";
Mediated A-to-1 Pre-mRNA Editing.";
G.: SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
C.: SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR GO: GO:0016011; C:integral to membrane; IEA.
GO: GO:0005210; F:extracellular ligand-gated ion channel activity; IEA.
GO: GO:0005210; F:extracellular ligand-gated ion channel activity; IEA.
GO: GO:000510; F:extracellular ligand-gated ion channel activity; IEA.
GO: GO:0005210; F:extracellular receptor activity; IEA.
GO: GO:0005210; F:extracellular ligand-gated ion channel activity; IEA.
GO: GO:0005210; F:extracellular receptor activity; IEA.
GO: GO:0005210; Neur channel activity; IEA.
DR GO: GO:0002531; Neur chan LBD: 1.
R Fam; PPGOS31; Neur chan LBD: 1.
R Fam; PPGOS32; Neur chan LBD: 1.
R Fam; PROS32; Neur chan memb; 1.
R FAM; FROS22; Neur chan memb; 1.
R FAM; FROS22; Neur chan memb; 1.
R FRIMTS; PRO0222; Neur chan memb; 1.
R FRIMTS; PRO0222; NEURCHANNEL.
DR FRIMTS; TIGRO0860; LIC; 1.
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LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                      DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                        DEGEDGTYHTSVVVKHGGSCLYVPPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQL
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                  YENCIMEWYASSVULTVVVLNYHHRTADIHEMPPWIKSVFLOWLPWILRMGRDGRKITRK 362
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Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor subunit Dalpha6 precursor.
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494
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Signal; Receptor.
SIGNAL
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29
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                          62
                                                                                                                                LQQIIDVDEKNQILTTNAMLNLEWNDYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSA
                                                                                                                                                                                                                               247 NLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGT
                                                                                                                SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                  LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                                                                                                                                                                                                                  DEGPDSTYPTNVVVRNNGSCLYVPPG1FKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                                                                                                                                                                   DLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNÇCPEPYIDITFAVVIRRKTLYYFF
                                                                                                                                                                                                                                                                                  243 NLIVPCVLISSWALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGT
                                                                                                                                                                                                                                                                                                                                                                                                                     367 PARVP-PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------HSCFGVDY-BLSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLI
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEQUENTS FACURE AND THE PURMED-11973307;
Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Grauso M., Reenan Dalpha7, in Drosophila melanogaster Identify a Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing.";
Genetics 160:119-1333 (2002).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
ENBL; AR321448; AAM13395.1; -.
FlyBase; FBGN0032151; nAcR-alpha-30D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type IV.
                                                                                         25;
                                                                  494;
PROSITE; PS00236; NEUROTR ION CHANNEL; 1. Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-070-2002 (TrEMBLrel. 21, Created)
01-0707-2002 (TrEMBLrel. 21, Last sequence update)
01-0707-2003 (TrEMBLrel. 24, Last annotation update)
01-0707-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinia cactylcholine receptor Dalpha6 subunit variant ty
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                  Length
                                                                                         83; Indels
                                       B46EBEDA63A92942 CRC64;
                                                               DB 5;
                                                               Score 1790.5; DB 5,
Pred. No. 1.6e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 AA.
                                                                                       53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 IFTLFTIIATLAVLLSAPHIMV 495
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                                      494 AA; 56095 MW;
                                                                67.2%;
                                                                           67.98;
                                                                          Local Similarity 67.9 es 341; Conservative
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                          Transmembrane
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                                                                Query Match
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                                                                            Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 WVLRMSRPGSATTPPPARVP-PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRY 410
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                                                                   IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 SHLAAPAGLILLICLLWPRGARC-GYHEKRLIHHLIDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- DEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LQQIIDVDEKNQILTTNAMLNLDEKNQLLITNLMLSLEWNDYNLRWNETEYGGVKDLRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 PHRLWKRDVLMYNSADEGFDSTYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 CEMKFGSWIYDGYQLDLQLQDEGGGDISSFVINGEWELIGVPGKRNEIYYNCCPEPYIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 CEMKFGSWIYDGNQLDLVLNSEDGGDLSDFITNGEWYLLAMPGKKNTIVYACCPEPYVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 TFAVVIRKTLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVA
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R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:005210; F:extracellular ligand-gated ion channel acti. . .;
R GO; GO:005216; F:ion channel activity; IEA.
R GO; GO:0005216; F:ion channel activity; IEA.
R GO; GO:0006811; P:neurotransmitter receptor activity; IEA.
R GO; GO:007268; P:synaptic transmission; IEA.
R GO; GO:007268; P:synaptic transmission; IEA.
R InterPro; IPR006201; Neur channel.
R InterPro; IPR006202; Neur channel.
R InterPro; IPR006202; Neur channel.
R Ffam; PF02312; Neur channel.
DR Ffam; PF02312; Neur channemb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PRINTS; PR00552; NRIONCHANNEL.
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01-JUN-2002 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last amnotation update)
01-JUN-2009 (TrEMBLrel. 2000)
01-JUN-2003 (TrEMBLrel. 2000)
01-JUN-2009 (TrEMBLrel. 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 509;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.6%; Score 1774; DB 5; 66.0%; Pred. No. 6.9e-164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           523 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Ionic channel; Postsynaptic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaricy coses 341; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLIVECVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNIVAESMPTTSDAVPLIGV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 TILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-PPPDLELRERSSKSLLANVLDIDDD 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 MPPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDDD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMQIIDVDEKNQLLITUIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEGFDSTYPINVVVRNNGSCLYVPPGIFKSŢCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----HSCFGVDY-ELSLILKEIRVIT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHLAAPAGILLILICLIMPRGARC-GYHEXRLLHHLLDHYNVLERPVVNESDPLQLSFGLT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLVLNSEDGGDLSDFIINGEWYLLAMPGKKKNTIVYACCPEPYVDITFTIQIRRRTLYYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-1 Pre-mRNA Editing."; Genetics 160:1519-1533 (2002).
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL, AF321449; AAM13396.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLPASLSLFVLLIFLAIIKESCQCPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 NLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21969411; PubMed=11973307;
Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
                                                                                                                                                                                                                            FlyBase; FBgn0032151; nAcR-alpha-30D.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:003054; F:ion channel activity; IEA.
GO; GO:0006611; F:ion transport; IEA.
GO; GO:0007268; F:synaptic transmission; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            523 AA; 59110 MW; 1C200AF74F87F841 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.4%; Score 1769; DB 5;
64.4%; Pred. No. 2.2e-163;
tive 53; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan LBD.
InterPro; IPR006202; Neur_chan LBD.
Pfam; PF02931; Neur_chan LBD; 1.
Pfam; PF02932; Neur_chan LBD; 1.
Pfam; PF02932; Neur_chan memb; 1.
PRINTS; PR00252; NEIONCHANNEL.
IIGR0860; LIC; ILC; ILC; ILC; PR051718; PS00236; NEUROTR_ION_CHANNEL, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 FRHPQAQQPQCCRYYRGGEENGAGLAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 342; Conserv
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RX ARAIN=Bergetgeley;
RXARN=Bergetgeley;
RXARN=Bergetgeley;
RX Adams R.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RADAM=SERGEGE,
RADAMS C.C. Celniker S.E., I. P. W., Hoskins R.A., Galle R.F.,
Guccoge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutron G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,
RADAMS R.M., Basul A., Baxendale J., Baraktaroglu L., Beasley E.M.,
Ballew R.M., Basul A., Barandari B.P., Bhandari D., Bollahakov S.,
RADEON R.Y., Bennos P.V., Berman B.P., Bhandari D., Bollahakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RADORON R., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P.,
RADUDIN R., Gabley S., Dalike C., Davensport L.B., Davies P.,
RADUDIN R., Ganger G.C., Ferraz C., Gun P., Harris M.,
RADUDIN R., Goore F., Gorrell J.H., Gu Z., Gun P., Harris M.,
RADUDIN R.J., Brangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RADUDIN R.J., Harvy D., Helman T.J., Herrandez J.R., Houck J.,
Adali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Jalai M., Kalush F., Karpen G.H., Ke Z., Kemnison J.A., Ketchum K.A.,
Jalai M., Kalush F., Karpen G.H., Ke Z., Kemnison J.A., Ketchum R.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Liu X., Mattei B., McIntoen T.C., Morris J., Moshreron D.,
RA Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshreron D.,
Rader R., Leat Y., Levtlesky A.A., Li J., Li Z., Ling Y., Welberson D.,
Rader R., Benn R.A., Now M., Murphy L., Muzny D.M., Nelson D.E.,
Reinert K., Remington K.A., Mixon K., Winsskern D.R., Pacleb J.H.,
Rader R., Tector C., Turner R., Venter E., Wang X.,
Rube B.C., Siden-Kiamos I., Simpson M., Strong R., Smith T.,
Rube R., Tector C., Turner R., Venter E., Wang X., Zhu S., Smith H.O.,
Rader R., Benn R.A., Worley R., Worley K.C., Wu D., Yen R.,
Rube B.C., Sanders R.W., Rolling M., Zhong M., Zhong W., Zhong R., Weinstech B., Rube B.C., Sanders R., Shong R.M., Wordage T., Worley K., Strong R., Sho
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Brans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Branson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

An Carlson J.W., Center A., Champe M., Davemport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

An Gonzalez M., Hookins R.A., Hoskins D., Moshnefi A.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

Millosh T.C., Moy M., Murphy B., Nelson C., Pelson K.A., Nunco J.,

Ancleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

T. "Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                  CG4128 protein.

NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropada; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                               Last sequence update)
Last annotation update)
554 AA.
                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:2185-2195(2000).
                                                                       13,
                                                                                                                                                  (TrEMBLrel.
                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley;
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                                                                           01-MAY-2000
                                                                                                               01-OCT-2002
   HID DATA BERNARA BERNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 LQQIIDVDEKNQLLITNLWLSLEWNDYNLRWNETSYGGVKDLRITPNKLWKEDVLMYNSA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYRGGEENGAGLAA-----HSCFGVDY-ELSLILKEIRVITDOMRKDDEDADIS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 ----GSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADDEAELI 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLQLQDEGGGDISSFVTNGEWELIGV-PGK--------RNEIYYNCCPEPYIDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B. Carlson J. W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%; Score 1484.5; DB 5; Length 554; 53.6%; Pred. No. 1.3e-135; Length 554; ive 53; Mismatches 98; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Figure (SEP-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; AE003626; AAF52817.2; -...

EMBL; AE003626; AAF52817.2; -...

R 19/Bases; FEBRO032151; hack-alpha-30D.

GO; GO:0016020; E:extracellular ligand-gated ion channel acti

R GO; GO:0036529; F:extracellular ligand-gated ion channel acti

R GO; GO:0036529; F:on transport; IEA.

InterPro; IPR006201; Neur_channel.

R InterPro; IPR006201; Neur_channel.

R InterPro; IPR006202; Neur_channel.

R InterPro; IPR006029; Neur_channel.memb.

R Pfam; PF02931; Neur_channel.memb.

R Pfam; PF02931; Neur_channel.memb.

R Pfam; PF02931; Neur_channel.memb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRODES; NRICONCHANNEL.
TIGREAMS; TIGRO0866; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
SEQUENCE 554 AA; 63236 MW; D6C63EB7F5B32A35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 53.68
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 [4]
SEQUENCE FROM N.A.
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310 ATVWVLQYHYHDPEGGKMPKWTRVVLLNWCAWFLRMKRPGEDKVRPACHNKOPRSSLSSV 369
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100 RMKELELKERSSKSLLANVLDIDDDFRHTIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                      IIATLAVLLSAPHIMV 495
                                                                                                                                                                                                                    (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423
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                                                                                                                                                   SEQUENCE FROM N.A., Matthews B.B., Bayraktaroglu L., Campbell K., Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Tradecky P., Huany Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Wunggall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALLGFTLPPDSGEKLSLGV---
Phouanenavong S., Pittman G.S., Furi V., Richards S., Scheeler F. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003626; AAN10709.1; -...

EMBL; AE003626; AAN10709.1; -...

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005230; F:extracellular ligand-gated ion channel acti

GO; GO:0005230; F:extracellular ligand-gated ion channel acti

GO; GO:0005230; F:extracellular ligand-gated ion channel acti

R GO; GO:0006811; P:ion transport; IEA.

R InterPro; IPR00620; Neur_channel.

R InterPro; IPR00620; Neur_chan.LBD.

R InterPro; IPR006029; Neur_chan.LBD.

R Pfam; PF02931; Neur_chan.LBD; 1.

R PRINTS; PR00252; NRIONGANNEL; 1.

R PRINTS; PR00252; NRIONGANNEL; 1.

R PROSITE; PS00236; NRIONGRANNEL; 1.

R SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;
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52.2%; Pred. No. 1.4e-124;
tive 56; Mismatches 108;
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Matches 290; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132
-GSQTAIGSSASFGRPTTV 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLDEGGGDISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Zirger J.M., Boyd R.T.; Zirger J.M., Boyd R.T.; "Cloning and expression of zebrafish neuronal nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor alpha 7 subunit.
Brachydanio rerio (Zebrafish) (Bunio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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BMBL; AY247962; AA0391913.1; -.

BMBL; AY247962; AA0391913.1; -.

GO; GO:0016620; C:membrane; IEA.

GO; GO:0016230; F:extracellular ligand-gated ion channel acti. .;

R GO; GO:001681; F:neurotransmitter receptor activity; IEA.

R GO; GO:000681; P:neurotransmitter receptor activity; IEA.

R GO; GO:000681; P:neurotransmitter receptor activity; IEA.

R InterPro; IPR00620; Neur channel.

R InterPro; IPR00620; Neur channel.

R Pfam; PF02931; Neur chan LBD; 1.

R Pfam; PF02932; Neur chan LBD; 1.

R PRINTS; PR00252; NRIOMEMANREL.

R TIGREPANS; TIGR0860; LIC; 1.
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al Similarity 50.0%; Pred. No. 5.2e-115;
247; Conservative 87; Mismatches 133; Indels
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DINISPGVAQSTNGNLLYI--GFRGMDTIH-YATSPDSGVICSRLVATGEEDVLLPGAQA 426
                                                                                                                                                SSVSSSGPGETELSKILDEVRYISKRFRDQDEEDTVCNEWKFAASVIDRLCLMAFSLFII 486
DLELRERSSKSILANVLDIDDDFR----HPQAQQPQ----CCRYYRGGEEN----GAGL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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SEQUENCE FROM N.A.
Jones A.K., Elgar G., Sattelle D.B.;
"The nicotinic acetylcholine receptor gene family of the pufferfish,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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44.7%; Pred. No. 4.7e-113;
ive 86; Mismatches 126; Indels 92
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor alpha 7b subunit (Fragment)
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EMBL; AY298752; AAP57216.1;
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Db 421 NISTGPPRVAGSPPPHLPSQFCSSPPPPASNMDTGCPSTVSSGGGGGGG---GGGLGGCS 477

Qy 426 CFGV-DYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATL 484

Db 478 ASAVGPPHALIEEVRFVADRFREQDEVSGAADQWKFAGAVIDRLCLVAFSVFNIICTI 537

Qy 485 AVLLSAPHIM 494

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Db 538 SILMSAPNFV 547
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Search completed: May 7, 2004, 11:38:38 Job time : 33.1579 secs This Page Blank (uspto)

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                 Copyright
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protein - nucleic search, using frame_plus_p2n model
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; Search time 3463.3 Seconds
(without alignments)
4276.744 Million cell updates/sec 8, 2004, 11:50:34 US-09-303-232-4 May Title: Perfect score: Run on:

2665 1 MGGRARRSHLAAPAGLLLLL......LFTIIATLAVLLSAPHIMVS 496 0.5 BLOSUM62 Xgapop 10.0 , Xgapext C Ygapop 10.0 , Ygapext ( Fgapop 6.0 , Fgapext Delop 6.0 , Delext Scoring table: Sequence:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

em\_estba:\*
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em\_htc:\*
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29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   | Description    |        | 32313 GRIGIZO | 01 901345<br>73 Homo 6 | 2240 | 51730 Mus | 30415 Mus | 753.TA 9900 | 49722 Mils | N Z | Mils | าก       |          | AGENC    | _        | Mus      | Mus      | Mus      | 2877 Pan   | 228 Mus   | CD013800 00130014 | 7 Min a  | 1 Dan tro | Mus      | 14 Pan tro | 5 9013   | 902 9013 | CD013903 90134855 | 391 9013 | 54 Mus   | 571 Mus  | 68 Mus mus | 1 1       | ) t      | CD013888 9013880 | K-ESTO | 27 Homo san | 44 Mus m | 5337 UI-M | 8211 Droso | 7974     | 3676 Drosonh | 7105 Min 2017 | 107/0F |
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|   |                |        | 10            | AY402873               | 5349 | 5173      | 041       | 0299        | 1972       | 4   | 0287 | AY402878 | AY402876 | BU915857 | AY406230 | AY406232 | AK029177 | AK080475 | A14028//   | AAC 34228 | CD013889          | AK030464 | AY406231  | AK081254 | AY402874   | CD013905 | CD013902 | CD013903          | CDOISB9I | AK087554 | AKU1/5/1 | n ~        | BII149265 | A1292581 | 88               | 9      | 1132        | 313      | 1533      | 1000E      | AK047974 | OHO          | AY407186      | 1      |
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## ALIGNMENTS

RESULT 1 BG632919/c

LOCUS

GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. BG6322919.1 GI:13758409 ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION

Drosophila melanogaster (fruit fly) Drosophila melanogaster Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

284

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/mol trype="mrs." | Jan. | Jan
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90134548 Single gene library Homo sapiens CDNA, mRNA sequence.
CD013901
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
1 (bases 1 to 2296)
10.P., Fug.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
Au-Young, J. and Stuve, L.L.
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                                                                                                                        165 GGAACTTATTTCAATTGCATTATGTTTATGGTGGCCTCATCAGTTGTGTCACCATACTT
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GTCCTCAATTATCATAGAAATCCAGATACGCATGAAATGAGTGAATGGGTA-----
                    465 GGCGAATGGGACTTGTTAGGTGTGCCCGGTAAACGAAATGAAATTACTGC
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                                                                                                                                                                                               PhePheAsnLeulleValProCysValLeulleAlaSerMetAlaLeuLeuGlyPheThr
205 GlyGluTrpGluLeuIleGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCys
                                                                                                ProGluProTyrileAspileThrPheAlaValValIleArgArgLysThrLeuTyrTyr
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Conservative:
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316 Porter Drive, Palo Alto, CA 94304,
Tel: 650 621 8639
Fax: 650 621 8965
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    Location/Qualifiers
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Unpublished (2003)
Contact: Jin, P.
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51 ATAGTTTTATAT 40
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                                                                                                                                                                                                                         Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyademylated. The resulting PollyT sequence has been removed. hit
genomic AE003511: arm:X [18792641,19136447]
estimated-cyto:18A3-18C6: 04/10/2001
Plate: GH.161 row: C column: 2
High quality sequence stop: 784.
Location/cualifiers.
rce
| 1.885/Qualifiers|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Gex. male and female"
/ Gev stage="adult"
/ lab_host="DHS - alpha"
/ clone | lib="GHD brosophila melanogaster head poT2"
/ note="Organ: head, Vector: poT2; Site 1: EcoR1; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into poT2.
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                                  T. (bases 1 to 885)
Tarvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Other ESTs: GH16126.5prime
Contact: Stapleton, M.
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/mol type="mRNA"
/db xref="taxon:7227"
/clone="GH16126"
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Matches:
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          Ephydroidea; Drosophilidae; Drosophila
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                                  | RESULT 4 AK053497 LOCUS DEFINITION | ACCESSION                                                               | KEYWOKDS<br>SOURCE<br>ORGANISM                                                                                           | REFERENCE<br>AUTHORS<br>TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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| gene <1>1436<br>/gene="CHRNA3"<br>/locus_tag="HCM1369"                                                                                       | Alignment Scores:  Pred. No.:  Score:  Score:  Percent Similarity:  Describent Similarity:  29.  Conservative:  Conservative:  Mismatches:  153  Query Match:  29.  Indels:  6                                                           | -09-303-232-4 (1-496) x AY402873 (1-1436)<br>28 AlaArgCysGlyTyrHisGluLysArgLeuLeuHisHisLeuLeuAspHisTyrAsnVal 47 | GCCAGGGCCTCAGAGGCTGAGCACCGTCTATTGAGCGGCTGTTTGAAGATTACAATGAG LeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluArgProValValAsnGluSerAspProLeuGluargProValValAsnGluSerAspProLeuGluArgProValValAsnGluSerAspProLeuGluArgProValValAsnGluSerAspProValValAsnGluSerAspProLeuGluArgProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAsnGluSerAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspProValValAspP | 63 ATCATECGGCCTGTGGCCAACGTGTCTGACCCAGTCATCCATTTCGAGGTGTCCATG 122 68 MetGlnIleIleAspValAspGluLysAsnGlnLeuLeuIleThrAsnIleTrpLeuLys 87 123 TCTCAGGTGGAAGGAAGAAGAAGAAGAAGAAGGAAGCAACTAGTGGCTCAAG 182 | LeuGluTrpAsnAspMetAsnLeuargTrpAsnThrSerAspPheGlyGlyValLysAsp | 108 LeuargvalProProHisArgLeuTrpLysProAspValLeuMetTyrAsnSerAlaAsp 127<br>                              | GluGlyPheAspSerThrTyrProThrAsnValValArgAsnAsnGlySerCysLeu            | TyrValProProGiventontontontontontontontontontontontonton             |                                    | Oy 188 LeuGlnLeuGlnAspGluGlyGlyGlyAspIleSerSerPheValThrAsnGlyGluTrp 207 | 208 GluLeuileGlyValProGlyLysArgAsnGluileTyrTyrAsnCysCysProGluPro 227 :::                                                 | OY 228 TYrIleAspileThrPheAlaValVallieArgargLysThrLeuTyrTyrPhePheAsn 247                                                                                                                                                                                              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                                                                                                                           | Oy 288 ASDMetValAlaGluThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyr 307 | 308 PheAsnCysIleMetPheMetValAlaSerSerValValSerThrIleLeuIleLeuAsn                                                                                                                                                   |

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MRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKESCKIDVTYF
PFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEIKYNCC
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatus, N., Hiramoto, K., Hiracka, T., Hirozane, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kotoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Rokanura, M., Nishi, K., Nomura, K., Numazaki, A., Murata, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takada, Y., Tagami, M., Tagawa, A., Takahashi, F., Takahira, S., Muramaka, T., Tanaka, T., Takahira, T., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (Croup, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Sanogas, 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, 79-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation Nature 470, 563-573 (2002)

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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection
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Please visit our web site for further details.
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/db_xref="MGI:2425288"
/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/db_xref="GI:26343495"
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/strain="C57BL/6J"
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WVKAVFLNLLPRVMFMTRPTSTEEDAPKTRNFYGAELSNLNCFSRADSKSCKEGYPCQ
DGTCGYCHHRRVKI SNFSANLTRSSSSESVDAVLSLSALSPEIKEAI QSVKYIAENMK
AQNVAKEI QDDWKYVAMVI DRIFLWVFILVCILGTAGLFLQPLMARDDT"
EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLPSDCGEKVTLCISVLLS
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

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R dacch,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiracka,T., Hirocane,T., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakai,C., Sakai,T., Tanaka,T., Tanaka,T., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takacha,Y., Tanaka,T., Tomaru,A., Takahashi,F., Takaku-Akahira,S., Takacha,M., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
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                                                                   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fuliwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIXEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIXEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Lastitute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseges.riken.go.jp, REL:kttp://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                        The RIKEN Genome Exploration Research Group Phase II Team and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
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/strain="C57B1/6J"
/db.xref="RANTON DB:D130068A06"
/db_xref="MG1:2420066"
/db.xref="MG1:2420060"
/db.xref="taxon:10000"
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/clone_lib="RIKEN full-length 6/dev_stage="12 days embryo"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
LeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGlu 292
                                      GTGACGCTCTGCATCTCCGTGCTCCTCTCCCTGACGGTCTTTCTCCTCGTGATCACCGAG
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High-efficiency full-length cDNA cloning
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TGGAAGTAIGTTGCCATGGTGATTGATCGCATTTTTTCTCTGGGTTTTTCATCCTGGTGTGC 1612
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GTCATGTTTATGACTAGGCCA-----ACCAGCACCGAGGAAGACGCCCCCAAAG 1255
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Sciurognathi, Muridae, Murinae, Mus.
                                                  TACTCGCTATACATTCGCCGCCTGCTGTTCTACACCATCAACCTCATCATTCCGTGC
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3126 bp mRNA linear HTC 19-SEP-Missurgulus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730007P14 product:NBURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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High-efficiency full-length cDNA cloning
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Mus musculus (house mouse)
Mus musculus
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Mammalia; Butheria; Rodentia
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                                    /protein_id="BAC34740.1"
|db_xref="G1:26342156"
|translation="MGVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFEDYNEII
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|GCTAACGTGTCCATCTGTCATCAGTTTGAGGTGTCTATGTCTCAGCTGGTGAAG 370
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/note="putative"
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QGVEFMRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKI
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3103. 3108
                                                                                                                                                        /protein id="FAC37909.1"
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                       /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR[AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497) butative"
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L. Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genome Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.go.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonake, S., Ishikawa, T., Tamaka, T., Matsuura, S., Kawai, J., Nokazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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/clone Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="7 days neonate"
                                                                                                          genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3126)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RIKEN Genome Exploration Research Group Phase II Team and the
           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and Subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium and the RIKEN Genome Exploration Research
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/strain="C57BL/6J"
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/tissue type="NEUROBLASTOMA COT 50-NORMALIZED" /clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and cloned into the Not I and stees of the pcMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                          was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7646.r For more information about this cluster, see
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                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODD007CH03QPl&cluster=7646.r. Contac
cgi-bin/cluster.cgi?seq=CSODD007CH03QPl&cluster=7646.r. Contac
Feng Liang Email : fliangalifecch.com/URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD007CH03QPl.
Location/Qualifiers
                                                                                      Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 19 91006 EWRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                    CCGGCCTACAAACATGAAATCAAGTACAACTGCTGTGAGGAGATCTACCAAGACATCACC
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,

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Submitted (16-JUD-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="spinal cord"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASTN, 99%, match=1498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                the FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                              Team and
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                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection
                                                                                              ΙΙ
                                                                                              Group Phase
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/db_xref="MGI:2417229"
/db_xref="taxon:10090"
                                                                                              The RIKEN Genome Exploration Research
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
245 PhePheAsnLeuIleValProCysValLeuIleAlaSerMetAlaLeuLeuGlyPheThr
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                                                                                                                                                 652 TCCTTGGATCTGCAGATGCAGGAG------GCAGATATCAGTGGCTATATCCCCAAT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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4046 bp mRNA linear HTC 20-SEP-2003 12 days embryo spinal ganglion cDNA, RIKEM Full-length ary, clone-13130/07121 product:cholinergic receptor, ta polypeptide 2 (neuronal), full insert sequence.
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                                        -caacccrcccrrc 1288
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                                                                                                                                                                                                                                                            ThrThrProProPlaArgValProProProAspLeuGluLeu 378
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                                                                                                                                 eArgCysValPheLeuTyrTrpLeuProTrpValLeuArgMetSerArg 358
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IleLeuIleLeuAsnTyrHisHisArgHisAlaAspThrHisGluMet 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="spinal ganglion"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev stage="12 days embryo"
                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4046)
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nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASIN, 99%, match=1498)
                                                                                                                                     The RIKEN Genome Exploration Research Group Phase II Team and
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sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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Please visit our web site for further details.
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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19
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                                                                                                                                                                                   ProGlySerAlaThrThrProProProAlaArgValProProProProAspLeuGluLeu 378
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritara, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargiil, M. Civello, D. R., Lu, F., Murphy, B., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1586 CIGITCCTCTGGATCTTTGTCTTTGTCTTTTGGGACCATTGGCATGTTCCTG 1642
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuCysLeullellePheThrLeuPheThrIleIleAlaThrLeuAlaValLeuLeu 488
   CTCGACGTGGTGGGAAAGTACCTCATGTTCACCATGGTGCTAGTCACCTTCTCC
                                                                                                                                     SerAspTrpIleArgCysValPheLeuTyrTrpLeuProTrpValLeuArgMetSerArg
                                                                                                                                                                                                                     ---CAACGCCTGCGCTTG
                                                                                                                                                                                                                                                     ArgGluArgSerSerLysSerLeuLeuAlaAsnValLeuAspIleAspAspAspPheArg
                                                                                                                                                                                                                                                                                                                     HisProGlnAlaGlnGlnProGlnCysCysArgTyrTyrArgGlyGlyGluGluAsn---
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerLeuIleLeuLysGlu------IleArgValIleThrAspGlnMetArgLys
                                                    ValValSerThrIleLeuIleLeuAsnTyrHisHisArgHisAlaAspThrHisGluMet
                                                                                                                                                                                                                                                                                                                                                                                   ---GlyAlaGlyLeuAlaAlaHisSerCysPheGlyValAspTyrGluLeu------
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Mus musculus CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence
                                                                                                                                                                                                                                                                                  1298 CGAAGGCGCCAGGGGAACGTGAGGGGGCAGGCACACTA
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Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                    1262 CCACGCCACCGCTGT------GCACGT
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320 153 380 497 213 557 233 617 253 677 273

| /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <li->1454 /gene="CHRNB4" /locus_tag="HCM1370"</li-> | Alignment Scores: Pred. No.: 8.33e-73 Length: 1454 Score: 905.00 Matches: 186 Percent Similarity: 59.78\$ Conservative: 92 Best Local Similarity: 40.00\$ Mismatches: 169 Query Match: 29 Gaps: 8 | 09 393-332-4 (1-496) x NY402878 (1-1454)  09 31 dlilusArgquelleHisHistolanday———HistyrAmValledGluArgpro 51   24 GAGSAGAAGCTGATGCATCCTCGAACAAACTGGTCACCACTGATCCCCCCA 83   25 ValValAmGlilusErAspPoteuGlilusErsPheGlyLeHittaWetGlilleHis 71   36 GCCACCACCTCCTCCCACCTCATCCCCTGACCTGACCACTCACT                                                                                                                                                                                                                           | /32 MGMICGIGCCICCCACCICCCIIGACAIICCCCICAIIGGCAAGIACCICIIIGIICACC |
|-----------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|
| Qy 314 MetValAlaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArgHisAla 333                                                     | Qy 354 LeuArgMetSerArgProGlySerAlaThrThrProProAlaArgValProProPro 373 :::     ::                                                                                                                   | 994 AspAspAspPehargHispColnAlaGINGInProGLAG9CgargTyrPyr 111  1086 AGCTCCAAGGAAGGCTACCCTGCCAAGATGGATGGATGTACTACCACCACGT 1142  412 ArgG1yG1yG1yG1uG1AmaG1yAlaG1yfeuhlaAlaHsSECCFPheGlyval 129  1143 AGGCTAAAAATCTCAAATTCAGTGCCAACCTCACAAGAAGCTCCAGACTTTT 1202  90 410 ArgG1yG1yG1uG1UGTAAFGTGCCAACCTCACAAGAAGCTCCAGACTTTT 1202  91 AAGGATAAAAATCTCAAAATTCAGTGCCAACCTCACAAGAAGCTCCAGACTTTT 1202  91 AAGGATAAAAATCTCAAAAATTCAGTGCCAACCTCACAAGAAGATCAGAGATTTGAGATTTG 1262  91 AAGGATACTTGATGTTGATTCATCTCACAACAAATCAAAAAAAA | •                                                                |

| source 11442 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1>1442 /gene <1>1442 /gene="CHRNB4" /locus_tag="HCM1370" | Alignment Scores: 6.24e-72 Length: 1442 Pred. No.: 895.50 Matches: 184 Percent Similarity: 58.60% Conservative: 92 Pest Local Similarity: 39.07% Mismatches: 163 Query Match: 33.60% Indels: 7 DB: 29 | US-09-303-232-4 (1-496) x AV402B76 (1-1442)  OY 34 GlubysAvgleueuissisischeudsgHistyrasivalleudluargero 51 24 GAGGAAAAGCTGACGCCTTCTGAACAAAACCCGTTACATAACCTGACCCCCA 83 25 ValvalasiclusExasperoteudleusSerbedlyteutlustewictalile 71 26 GCCACGGCTCCTGACGCTCATCTCCATCAAGCTGACTCCCCGGCCTATC (143 72 AspalasiclusExasperoteudleusSerbedlyteutlustewictalile 71 14 ACCTGAAAAGCTGACGCTCATCTCCATCACGCTGACTCCCCGGCCCAGCTTATC (143 72 AspalasiclusExasperoteudleusSerbedlyteutlustewictalile 71 204 GATTACCGCTGACACGCTCATCTCCACCAATGTCTGGCTGAACACGACTCTCT (143 205 ASPACAAGCTGACACACACTCATCACACACACACTCGGCTGAACACGACTCTCTCAGCGTTATC (143 206 GATTACCGCTGAACACACACACACACACACACTCGGCTGAAACACGACACACTCTCAGCTGAACACACAC | Db 732 AAGATGACATGTGGTGTGTGTGTGTGTGTGTTGTTCTTCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG                                                              |
|-----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| Qy       312 MetPheMetValalaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArg 331         Db       1                                              | Qy 352 TrpValLeuArgMetSerArgProGlySerAlaThrThrProProAlaArgValPro 371                                                                                                                                  | 09 388AlaAssValleuAsplleAspAspAspAspAspHstrolnAlaGinGin 404  1086 AGCAGCCCARCCARCCTCTATGGGAATTCCATGTACTTTGGAACCTCTCCCCGCACT 1145  405 PROGINCysCyaArgTyrTytArgGlyGliGiuAsnGlyAlaGlyGluchAaha 423  416 CCTAAGTCTGCAGTCAGTCAGCCACCGCAGCGCACCTCCCTGCCCTGCCCTGCTCCTGCTGCTGCTGCTGCTGC                                                                                                                                                                                                                                                                                                                                                                                                                           | Rockville, ND 20850, USA Rockville, ND 20850, USA This sequence was made by sequencing genomic exons and o them based on alignment. Location/Qualifiers |

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/clone lib=NUCHD XGC OO1"
/note="Vector: pCMV-SPORT6; Site 1: Not1; Site 2: Sal1;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 MetLysPheGlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGlnAspGlu 193
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                                                                                                                                                                                                                                                                                                                                                                                                                      100 TATTIGCAGIGGAACAIGICIGAAIACCCIGGGGIAAAAAAIGITICGITITICCAGAIGGA
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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1 (bases 1 to 922)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
ToNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information of the count through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LiAMM4228 row of column: 14
High quality sequence stop: 746.
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Homo sapiens CHRNAl gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1374)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferritera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. P. Adams, M.D. and Cargill, M. P. Inferring nonneutral evolution from human-chimp-mouse orthologous
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|CTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGGCCAGTGGAAGACCAC 135
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                                                                                                                                                                                                                                                                                                                                 Submitted (16-NNV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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TrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspSerThrTyrPro 135
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                ThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProProGlyIlePheLys
                                                                                 496 CTGGGCACCTGGACCTATGACGGCTCTGTGGTGGCCATTAACCCGGAAAGTGAC---CAG
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                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Li 1374)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wangog,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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                                                                                                                                                                                                                                                                                               Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Mus musculus CHRNA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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7, 2004, 12:59:49; Search time 5953.59 Seconds (without alignments) 10942.062 Million cell updates/sec using sw model nucleic search, May OM nucleic Run on:

1 atggcccctatgttggcggc......acccgcatatcatcgtgcaa 1503 US-09-303-232-5\_COPY\_95\_1597 1503 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6940544 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

em\_htg\_inv: \*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |        | o <sup>3</sup> t |        |    | SUMMARIES |                    |
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| 14            | 535    | 35.6             | 1683   | ო  | DME554210 | AJ554210 Drosophil |
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| 22            |        | 25.1             | 1916   | σ  | AF385585  | AF385585 Homo sapi |
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| 25            |        | 25.0             | 2106   |    | RATNARAD  | L31619 Rattus ratt |
| 26            |        | 25.0             | 0      | 10 | S53987    | S53987 nicotinic r |
| 27            | 375.6  | 25.0             | 2087   | 9  | HSARA7A   |                    |
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| 29            | 7      | 24.9             | വ      | 9  | AX054567  |                    |
| 30            | $\sim$ | 24.9             | ထ      | 9  | AR282833  | m                  |
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| 32            | 374    | 24.9             | œ      | σ  | HSU62436  | U62436 Human nicot |
| 33            | 37     | 24.9             | 0      | 10 | AF225980  | AF225980 Mus muscu |
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| 36            | 73.    | 24.9             | œ      | ص  | AR055255  | AR055255 Sequence  |
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| 38            | 373.6  | 24.9             | 1876   | 9  | AR173187  | 7 Sequenc          |
| 39            | 73     | 24.9             | œ      | 9  | AR224030  | 30                 |
| 40            | 72.    |                  | ഹ      | 9  | AX054575  | 575                |
| 41            | 372.4  | 24.8             | S      | 9  | AX054577  | 7                  |
| 42            | 372.4  |                  | 1848   | 10 | MUSNARS   | Σ                  |
| 43            | 371.8  | 24.7             | φ      | Ŋ  | AY298753  | Takifug            |
| 44            | 370.8  | ⁴.               | ഗ      | 9  | AX054579  | S                  |
| 45            | 365.8  | 24.3             | 1542   | Ŋ  | AY299466  | AY299466 Takifugu  |

ALIGNMENTS

AF143847 3029 bp mRNA linear INV 27-MAY-1999 Heliothis virescens putative nicotinic acetylcholine receptor alpha 7-2 subunit mRNA, complete cds. Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuoidae; Heliothinae; Heliothis.

1 (bases 1 to 3029)
Schulte,T., Oellers,N. and Adamczewski,M. AF143847 AF143847.1 GI:4895006 DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS RESULT 1 AF143847 LOCUS

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Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha
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/db_xref="G1:000-wAPPMLAALALLALPVSEQSPHEKRLLNALLANYNTLERPVANE
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CDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEWYLLGMPGKKNTITYACCPEPYV
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HUVBETLPQVSDAIPLIGTYFNCIMFWVASSVVLTVVVLNYHRTADIHEMPQMIKSV
FLQWLPWILRMSRPGKKITRYTIMMYRRREIELKERSSKSLANVLDJDDDFRHGPP
PPNSTASTGWLGPGGSIFRTDFRRSFVRPSTWEDVGGGLGSHRELHLILRELQFITA
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/organism="Heliothis virescens"
/mol type="manna"
/db_xref="taxon:7102"
95. .1600
/note="hvnachra7-2"
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Unpublished
2 (bases I to 3029)
Schulte,T., Oellers,N. and Adamczewski,M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG,
                                                                                                                                                                                                                                                               /codon_start=1
/product="putative nicotinic
7-2 subunit"
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Best Local Similarity
Matches 1503; Conserv
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1 (Dases 1 to 3109)

2 Martin,A., Nadja,E. and Thomas S.

Nucleic acid encoding insect actyl choline receptor subunit Patent: JP 2000023680-A 3 25-JAN-2000;

BAYER AG

OS Heliothis virescens
PD 25-JAN-2000
PP 25-JAN-2000
PP 26-APR-1999 JP 1999118159
PR 04-MAY-1998 DE 19819829.9
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/mol_type="genomic DNA"
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E58348.1 GI:13019347
E2800023680-A/3.
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Heliothis virescens
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RMKKADEEAELI SDWKPPAMVVDRFCLFVFTLFTI I AFTVAVLLSAPHILVQ**
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Nucleic acids encoding acetylcholin-receptor subunits from insects
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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/db_xref="taxon:7102"
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/organism="Heliothis virescens"

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/ translation="MOSPHEASLEVILIFIAIIXESCOGPHEKRILINHILSTYNTL

ERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLMLSLEMNDYNLRWNETEYGGVK

DLRITPNKLMVEDPUMYNSADREGNGTYHTNIVVKHGSCGLVYPPAPIRKSTGWDITW

FPPDDQHCEMKFGSWTYDGNLANSEDGGDGTSDFITNGEWYLLAMPGKKNTIVYA

CCPEPYVDITFIQIRRRILYYFFNLIVPCTYLISSMALLGFTLPPDSGEKLTIGVTIL

LSTLYFRINJVARTLEPQVSDAIPLGTYYPRCTILISNRWKESLELKERSSKSLLANVLDIDD

PPWTKSVFLQMLPWILRMGRPGRKITRKTILLISNRWKESLELKERSSKSLLANVLDIDD

DFRHTISGSGTAIGSSBASFGRPTTVERHITAIGCNHVDLHILIKELQFITARMRKADD

EAELIGDWKEAAMVVDRFCLIVFTLFTIAIVTVLLSAPHIIVQ"
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Movel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
Genetics 160 (4), 1519-1533 (2002)
     nicotinic acetylcholine receptor Dalpha6 [ (nAcRalpha-30D) mRNA, complete cds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OX1 3QX, UK
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compared to the sequence deposited in GenBank Accession
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                                                                                                                                                                                        Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor; alternatively spliced; contains exons 3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="nicotinic acetylcholine receptor Dalpha6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ion channel; neurotransmitter transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 770.2; DB 3; Length
Pred. No. 1.1e-193;
0; Mismatches 393; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                    (fruit fly)
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to the sequence deposited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79. .1863
| qene="nAcRalpha-30D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="nAcRalpha-30D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="embryo"
1. .2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Hum
  melanogaster n:
riant type III
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                                                                                                                                                                    Drosophila melanogaster
                                                                                                                GI:20152848
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Drosophila melanogaste
subunit variant type I
alternatively spliced.
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  DEFINITION
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TITLE
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JOURNAL
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MEDLINE
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/db_xxef="di:20152845"

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ERPVANSEDLEWKEGHTLQQIIDVOEKNQIITTNAMLNLEWNDYNLRWNETEYGGVK

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PPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA

CCPEPYYDITFTI GIRRATLYYFENLIVPCVLISSMALLGFTLPPDSGEKLTLGVTI

ISLTYPLNATRTLPQVSDA.PLLGTYFFNCINFWASSVYLTWVLIVYVHRTADIHEM

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PPRIKSGGTALGSSAFGRPTTVEEHHTAGCNHVOLHILLKELQFITARNRKADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="nAcRalpha-30D"
/note="results in isoleucine to methionine substitution;
compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compared to variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 AGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 IGIGGAAGCCGGACGTCCTTAIGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGGTGGAACGACGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCCAACAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="nAcRalpha-30D"
/note="results in asparagine to glycine substitution;
compared to variant clone"
/replace="gg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTGGCGGCCTTGGCTGCTTTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="nacRalpha-30D"
/note="results in asparagine to serine substitution;
compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="nAcRalpha-30D"
/note="compared to variant clone"
/replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone'
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Pred. No. 1.5e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nAcRalpha-30D"
/note="compared to variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in serine
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gene="nAcRalpha-30D"
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1605. .1607
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1683
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Best Local Similarity 70.1
Matches 1046; Conservative
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Product="nicotinic acetylcholine receptor Dalpha6 subunit variant type 1"
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Buskaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophiladae; Drosophila.

I (bases 1 to 2023)
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Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
                1490 AGGAGCTGGAGCTAAAGGAGCGCTCCTCCAAATCCCTGGTGGCCAATGTCCTCGACATCG
                                                                                                                                                                                                                                                                                                                            ricasegacearcacacearcacearcacaarcacaagarcircarciaaircircaaag
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                                                                                                1151 ATGATGACTTCAGACACGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGG
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/note="results in glycine to serine substitution, compared
to variant clone"
treplace="a"
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LSLIVTELNIVARSMPTTSDAVPLIGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEM
PPWIKSVFLQWLPWILMRDERKITRKTILLSNRMKELELKERSSKSLLANVLDIDD
DFRHTISGSQTALIGSSASFGRPTTVEEHHTAIGCNHKOLHLILKELQFITARMRKADD
BAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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ERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLMLSLEWNDYNLRWNETEYGGVK
DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHGGSCLYVPPGIFKSTCKMDITW
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Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mNNA Editing
Genetics 160 (4), 1519-1533 (2002)
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Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK
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                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2023)
  CGATTATTGCAACGGTTACGGTGCTCCTCCGCTCCGCACATAATCGTGCAA 1860
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/note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3b
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/product="nicotinic_acetylcholine
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Drosophila melanogaster
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/db_xref="GI:20152847"
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/mol_type="mRNA"
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/db_xref="taxon:7227"
/chromosome="2"
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/gene="nAcRalpha-30D"
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1. .2023
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subunit variant type II
alternatively spliced.
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Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WC1E 6BT, UNITED
KINGDOM
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Drosophila melanogaster (fruit fly)
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera, Endopteraygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/gene="nAcRalpha-30D"
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/product="nicotinic acetylcholine receptor subunit
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               /mol_type="mRNA"
/db_xref="taxon:7227"
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AATCGGAGCCCCTGGAGGTTAAGTTCGGACTGACGCTGCAGCAGATCATCGACGTGGACG 254
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Submitted (19-DEC-2003) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
reflect clone was sequenced as curracy, presence of a polyA tail and contiguity
or sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unsplaced precursor RNAs, and
reverse transcriptase errors that result in single base changes,
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
codna@fruitfly.berkeley.edu)

Location of codna@fruitfly.berkeley.edu.
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SSKSLLANVLDIDDFRHTISGSQTALGSSARFRPTVEBEHTAIGCNHKDLHLILK
ELQFITARNKKADDEAELIGDWKFAAMVVDRFCLIVPTLETIIATVTVLLSAPHIIVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLWLSLEWND
YNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYHTSVVVKHGGSCLYVP
PGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLSSEDGGDLSDFIINGEWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FLYBASE:FBgn0032151"
/translation="PFNPRATRYKQAKDMDSPLPASLSLFVLLIFLAIIKESCQGPHE
    1 (bases 1 to 1699)
Stapteton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
and Celniker, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 AGCGCCTGCTGAACCATCTGCTGTCCACCTACAATACGCTGGAGCGACCCGTGGCCAATG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTGGCGGCCTTTGGCTGCTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="mRNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/lose="nAcRalpha-30D"
/gene="nAcRalpha-30D"
/db_xref="FLYBASE:FBgn0032151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 747.8; DB 3;
Pred. No. 1e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAR82815.1"
/db_xref="G1:40216008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="nAcRalpha-30D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="GH15518p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Longest ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon start=2
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JOURNAL
         REFERENCE
                            AUTHORS
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VVLNYHHRTADIHEMPPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKE
RSSKSLLANVLDIDDDFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLIL
KELQFITARMRKADDBAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACG 130
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                                                                                                                                                                                                                                                                                                                                                                                                    /note="results in methionine to isoleucine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                             /gene="nAcRalpha-30D"
/note="results in arginine to histidine substitution;
compared to the sequence deposited in GenBank Accession
Number AB003626"
                                                                                                                                                                                                                                                                      /note="results in serine to asparagine substitution;
compared to the sequence deposited in GenBank Accession
Number AB003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGACGAGAAGAATCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTGGCGCCCTTGCTTGCTTTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 AATCGGAGCCCCTGGAGGTTAAGTTCGGACTGAGGCTGCAGCAGATCATCATCGACGTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590 AAAAGAATCAGATTCTGACCACAAATGCGTGGTTAAATTTGGAGGAGGAATCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTATAACCAATATATGGCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rcaraaccaarcrirgecrircerregagregaaccaacracaarcrececregaaraaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 GCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCCCAACAAGTTGTGGAAGCCGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  710 CGGAATACGGCGGGGTCAAGGATCTACGAATCACGCCCAACAAGCTGTGGAAGCCCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 TCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACCAGACCAACGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 TCAGAAGCGGCAGTTGCCTGTACGTGCCACCTGCATATTCAAGAGCACATGCAAGA
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Accession Number AE003626"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="compared to the sequence deposited in GenBank
Accession Number AE003626"
/replace="c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="compared to the sequence deposited in Accession Number AE003626"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.6%; Score 715.2; DB 3; 68.8%; Pred. No. 5.1e-179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="nAcRalpha-30D"
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                                                                                                                                                                                                                                                                                                                                                                                   'gene="nAcRalpha-30D"
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1728
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Matches 1058; Conserv
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                                                                                                        1390
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                        1472
                                                                                                                                                                                              1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein id="ANA13395.1"
//brotein id="ANA13395.1"
//brotein id="ANA13395.1"
//bb_xref="G1:20152851"
//translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLINHLLSTYNTL
BRPVANKSEPLEVKFGLTLQQIIDVDEKNQILTTNAMINLESKNQLLITNIMISLEBN
DYNLRAMETEYGGVKDLRITPNKLMKPDVLMYNSABGFPGTYHTNIVVKRSGSCLYV
PPGIFKSTCKNDITWPFPDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEM
YLLAMPGKKNTIVYACCPEPXVDITFTIQIRRRILYYFFNLIVPFVLISSMALLGFTL
PPDSGBKLITLGYTILLSLTVFTNLVBETLPQVSDAIPLGTYFNCIMPMVASSVVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear INV 29-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                      2068 bp mRNA linear INV 29-APR-20
nicotinic acetylcholine receptor Dalpha6
(nAcRalpha-30D) mRNA, complete cds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a, 3b
8b; contains two repeats of the functional domain loop
                                                                                                                                         AATTGCAATTTATTACGGCGGATGCGCAAAGCTGACGACGAAGCGGAATTGATCGGCG
                                                                                                                                                                                     ACTGGAAGTTTGCTGCGATGGTTGTTGATAGGTTTTTGCCTGTTCGTGTTCACACTTTTCA
                                                                                                                                                                                                                            ATTGGAAGTICGCGGCAATGGTTGTGAATAGATTTTGTTTAATTGTTTTCACGCTCTTCA
         TGGAAGACGTGGGCGGCGGGTGGGTAGCCATCGCGAGCTGCACCTCATACTGAGAG
                                                     TGGAGGAGCATCACACGCCATCGCCATCACAACAACATCTTCATCTAATTCTCAAAG
                                                                                                 AGCTGCAGTTCATCACGCCAGGATGAAGAAGGCTGATGAGGAAGCCGAGCTGATCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                     CAATCATCGCGACAGTAGCTGTCGTTATCGGCACCGCATATCATCGTGCAA 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="nicotinic acetylcholine receptor Dalpha6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:7227"
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L. .2068
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suso,M. and Sattelle,D.B.
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Drosophila melanogaster
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alternatively spliced.
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(db xref="G1:20152883"

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                                                                                                                2110 bp mRNA linear INV 29-APR-2002 nicotinic acetylcholine receptor Dalpha6 (nAcRalpha-30D) mRNA, complete cds,
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/product="nicotinic acetylcholine receptor Dalpha6 subunit
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receptor; alternatively spliced; contains exons 3a, 8a and
8b; contains two repeats of the transmembrane TM2 region"
                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaeret (11011 117)
Drosophila melanogaeret (11011 117)
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2110)
Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Dovel Putrative Nicotinic Aectylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify.
New and Highly Conserved Target of Adenosine Deaminase Acting on Genetics 160 (4), 1519-1533 (2002)
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/note="results in methionine to isoleucine substitution,
/ongrested to the sequence deposited in GenBank Accession
Number AE00366"
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/note="compared to the sequence deposited in GenBank
Accession Number AE003626"
/replace="c"
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Grauso,M. and Sattelle,D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford (30X, UK
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/organism="Drosophila
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379. .1950
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/gene="nAcRalpha-30D"
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/db xref="taxon:7227"
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1. .2110
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/map="30D1"
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subunit variant type V (
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alternatively spliced.
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TCAAACGTAGCGGCAGTTGTCTGTACGTGCCCCCTGGTATCTTCAAGAGCACATGCAAGA
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Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota, Metazoa; Arthropoda, Hexapoda; Insecta; Pterygota;
Eukaryota, Mediacoa; Arthropoda, Hexapoda; Insecta; Pterygota;
Noctucida, Noctuidae, Heliothinae; Heliothis.

[ bases 1 to 3629]
Schulte,T., Oellers,N. and Adamczewski,M.
Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Cell
than to other insect nicotinic acetylcholine receptor alpha
        CGACAACGTCGGATGCTGTTCCTCTTATAGGAGTTACAATTCTTCTATCGCTCACAGTGT 1309
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Schulte, T., Oellers, N. and Adamczewski, M.
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gene="nAcRalpha-30D"
/note="compared to the sequence deposited
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Hoeptera; Endoptery/gota; Lepidoptera; Glossata; Ditrysia;
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/db_xref="G1:4895005"
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Pred. No. 1.1e-141;
0; Mismatches 460; Indels 48
                                                            Bldg.
                                                                 AG,
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/organism="Heliothis virescens"
                                                                 Bayer
Direct Submission
Submitted (19-APR-1999) ZF-BTB,
51368, Germany
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Heliothis virescens
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Endopterrygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Heliothinae; Heliothis.

1 (Dases I to 3701)
Martin,A., Nadja,E. and Thomas,S.
Mucleic acid encoding insect actyl choline receptor subunit
Patent: JP 2000023680-A 2 25-JAN-2000;
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OS Heliothis virescens
BN 19 20023680-A/2
BD 25-JAN-2000
PF 26-APR-1999 JP 1999118159
PR 04-MAY-1998 DE 19819829.9
PI MARTIN ADAMUTSUBUSUKI, NADJA ERASU, THOMAS SCHULTE PC
C12N15/09, A01K67/033, C07K14/705, C07K16/28, C12N1/21, C12N5/10, C12Q1/68,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 575; DB 6; Length 3700; Pred. No. 1.1e-141; 0; Mismatches 460; Indels 44
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                                                                                                                                   'note="unnamed protein product"
      organism="Heliothis virescens"
                                  'mol_type="unassigned DNA"
'db_xref="taxon:7102"
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64.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGAGAGCTGCAGTTCATCACGGCCAGGATGAAGAAGGCTGATGAGGAAGCCGAGCTG 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIGAAGGAGATIAGAGICAICACAGAIGCGCAAGGACGACGAAGAIGCGGACAIT 1702
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Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WCLE 6BT, UNITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTCACAATCATCGCGACAGTAGCTGTCCTGTTATCGGCACCGCATATCATCGTG 1500
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                                                                                                                                                                                                                                                              1391 GTGCTGCGCATCTCACGGCCCGGCTCGCCG---ACGACGCCGCCGCCGCGCGTACCT
                                                                         GCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCATGG
                                                                                                                                           1331 GCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTGCCGTGG
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Drosophila melanogaster
Bukaryota; MetaZad; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

Millar,N.S.
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/mol_type="mRNA"
/db_xref="taxon:7227"
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0; Mismatches 460;
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/organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="teaxon:7102"
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KLSLGVTILLSLTVERLIMVAETWPATSDAVPLLGKYFRVIMFWASSVVSTILVLNYH
HRNPDTHEMSEWIRVIFLYWLPCILLRWQRPGQVGYECPPPPSSSSSSSGSGEKKQQIQN
VELKRSKSKSKLANVLDIDDPRCNHRCASATLPHQPTYYRTWYRQGDDGSVGFYGQN
GPVVJGRLHRAISHCLTSSLEYLLLKELMUITEQLKKEDBTSDITRDWKFAAMV
VDRLCLIIFTLIFTIIATLAVLFSAPHFIVSGVG"
          ALLDNYNSLERPVVNBSDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRW
NSSEFGGVRDLRIPPHRLWKPDVLMYNSADEGFDGTYATNVVVRNNGSCLYVPPGIFK
translation="MSFPQPHSLPEATANGGRMLVYGLGLLIMIPACAAGPHEKRLLH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGTGGTTCGCAATAATGGGAGCTGTCTGTACGTACGCGCCAGGTATATTTAAGTCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTGTGATATGAAGTTCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                 CCATTGCAACTGAGCTTCGGACTAACACTCATGCAGATTATCGATGTGGACGAAAAGAAT
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                subunit
                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                 Length 1683;
                                                                                                                                                            /gene="nAcRalpha-18C"
/product="nicotinic acetylcholine receptor
Dalpha7"
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                               Score 535; DB 3; I
Pred. No. 4.8e-131;
0; Mismatches 540;
                                                                                                                                        /gene="nAcRalpha-18C"
132. .1651
                                                                                                                                                                                                                                 35.6%;
larity 61.0%;
Conservative
                                                                                                                              26. .131
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                           Local Simines 942;
                                                                                                                              sig peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1111
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858
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                                                                                                                                                                                                                                                                                                         rcaditichercadecaracitetreiteraritarearadaanaeagaraegaradaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGATCACCAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTATAATGAAGAACACGAGGATGAGGGAGCTGGAACTGAAGGAGAGGTCGTCGAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1292 GCGACTTTGCCCCACCAGCCCACATATTACAGGACGATGTACAGGCAAGGGGATGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----CATCGCGAGCTGCACCTCATACTGAGAGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1412 TCCCACACCTGTCTGACATCCTCTGCGGAGTACGAACTGGCGCTGATACTCAAGGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGTTCATCACGGCCAGGATGAAGAGGCTGATGAGGAAGCCGAGCTGATCAGCGACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGTTTGCTGCGATGGTTGTTGATAGGTTTTTGCCTGTTCGTGTTCACACTTTTTCACAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTTGCTGCCATGGTCGTCGATCGTTTGTGCCTTATTATTTTTCACCTTGTTTACTATT
ACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCCGAGACCCTGCCACAGGTC
                                                      872 ACAATICTATTATCGCTTACAGTCTTCCTCAACATGGTGGCCGAAACAATGCCGGCGAC
                                                                                                                      TCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGCTAGCGTCG
                                                                                                                                                                               rccearecegracecreeredraaciarricaariecarrarerraregecerea
                                                                                                                                                                                                                                               TCTGTGGTACTGACTGTGGTGGTACTCAATTACCACCATCGAACAGCTGATATACATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1112 AGACCCGGCACAGGTTGGCTACGAATGTCCGCCGCCGCCCTCTTCTTCGAGTTCCTCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCGGCGAGAAGAAGCAACAATCCAAAACGTTGAGCTCAAGGAGAGGTCCTCCAAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCTGGCGAATGTTCTAGATATTGATGACTTCAGACACGGCCCTCCGCCTCCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 CTGCTGGCCAATGTGCTCGATATAGACGATGATTTCCGATGCAATCATCGATGTGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1352 AGCGTGGGACCCGTGGGACCAGCTGGTCCAGTTGTGGACGGGCGTTTGCACGAGGCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1186 AGTACTGCCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCCGCACGGATTTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTCGTTCGTCCGTCCGTCCACGATGGAAGACGTGGGCGGCGGCGGCTGGGTAGCCAC-
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2907 bp mRNA linear INV 29-APR-20 nicotinic acetylcholine receptor Dalpha5 mRNA, nAcRalpha-34E-A allele, complete co Pterygota; Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot
Bobptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

ಗ l\_ (bases 1 to 2907)
Grausco, N., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Submit Genes,
Novel Putative Nicotinic Acetylcholine Receptor Submit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing

116

1331

176

4,

Gaps

51;

1451

296

1391

236

1571

1631

476

1691

596

536

1751

1511

416

356

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AGGICCICACGAGAAGAGACTCCIGAACGCGTIGCIGGCGAACIACAACACCCTGGAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 ACCGGTGGCCAACGAGGGGAACCGCTAGAGGTCAGGTTCGGCTTGACCTTGCAGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1272 TCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTTAATGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 CATTGACGTGGACGAGAAGAATCAACTACTTATAACCAATATATGGCTGTCGTTGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1332 TATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGTGAAAACTGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAATGACTACAACCTGAGGTGGAACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1392 GAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 CACGCCCAACAAGTTGTGGAAGCCGGACGTCTTATGTATAATAGTGCTGACGAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1452 ACCGCCCCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1512 TGACGCCCCTACCAGACGAGGTGGTGCGGAACAACGGCTCGTGTCTATACGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 ACCTGGCATATTCAAGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1572 GCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGCTTCCCTTCGATGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 ACACTGTGATATGAAGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1632 GCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCTGGATTTACAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537 AAAAGATGAGGCGGCGGCGATCTATCGGACTTCATAACAAATGGGGGAGTGGTATCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1692 ACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCCAACGGCGAGTGGGAACTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597 AGGAATGCCAGGCAAAAAAAACACAATAACATACGCGTGCTGCCCCGAGCCCTACGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1752 GGGTGTGCCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCCGGAACCCTATATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     657 CGTCACCTTCACCATCATGATAAGAAGACGAACCTTGTACTACTTCTTCAACCTGATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcaccirceccarcarcecceaecaacacrerarrrrrrraaccrearcar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCITION OF THE CONTROLL OF THE CONTROL OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCGAGACCCTGCCACAGGTCTCCGACGTATCCCCCTGTTAGGGACGTACTTCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1992 recedadacaarecegeracriccarecegecearecegeracratarricaarre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     957 TCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2112 TCGAAATGCTGATACGCACGAAATGTCCGAATGGATACGCATCGTGTTTTTGTGCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1932 IGAAAATTATCGCTGCTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGT
                                       serine substitution;
                                                                                                                                                                                                          Length 2907;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                      Score 521.6; DB 3;
Pred. No. 1.9e-127;
0; Mismatches 519;
   /gene="nAcRalpha-34E"
/note="results in asparagine to
compared to B allele"
/replace="g"
                                                                                                                                                                                                          34.7%;
ilarity 61.8%;
Conservative
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                      924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
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                                                                                                                                                                                                          Query Match
Best Local
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DPLQLSFGLTLMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDRIPPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQC
REMFGSWYTDTOFQLDLQLOGDFGDDALSSYLNGBWBLLGVPGRRNBITYNCCPBYID
ITFAIIIRRYLLYYFFNIIPCVLLASMALLGFTLPPDSGEKLSLGYTILLSITYVFLN
MVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSEWIRIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCWLPWILRMSRPGRPITLEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDI
DDDPRHNCRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSST
EYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVL
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compared to B allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serine
                                                                                                                                                    Direct Submission
Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU,
University of Oxford, South Park Road, Oxford OX1 3QX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="nicotinic acetylcholine receptor Dalpha5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="ion channel; neurotransmitter transmembrane
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substitution; compared to B allele"
/replace="c"
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compared to B allele"
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/mol_type="mRNA"
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/note="compared to B allele"
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compared to B allele"
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="embryo"
1. .2907
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/allele="A"
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gene="nAcRalpha-34E"
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Grauso, M. and Sattelle, D.B.
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                               MEDLINE
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| 1065<br>2231                                     | 1106     | 1166                                                                  | 1215<br>2411                                      | 1274                                                       | 1325                                              | 1385<br>2591                                                                                                                        | 1445<br>2651                                                |                                                            |
|--------------------------------------------------|----------|-----------------------------------------------------------------------|---------------------------------------------------|------------------------------------------------------------|---------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|------------------------------------------------------------|
| GCCATGGATACTGCGAATGTCGAGGCCAGGAAGAAGATCACCAGGAAG |          | GGAGAGGTCGTCGAAGTCCTTGCTGCTGGCGAATGTTCTAGATATTGATGATGATTCTGAGACACACAC | CGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGGGACCT | GGGIGCTCAATATTCCG-CACGGATTTCCGTCGTCGTTCGTCCGTCCGTCCGTCCGTC | AGACGIGGGCGGGGCTGGGTAGCCACCATCGCGAGCTGCACCTCATACT | GAGAGAGCTGGAGTTCATCACGGCCAGGATGAAGAAGGCTGATGAGGAGCCGAGCTGATGATGATGATGATGAGAAATTCGCTTTATAACTGATCAGCTAACGTAAAGATGACGAGTGCGAATGACATTGC | CAGCGACTGGAAGTTTGGTGGATGGTTGTTGATAGGTTTTGCCTGTTCGTGTTCACACT | TTTCACAATCATCGCGACAGTAGCTGCTCGTTATCGGCACCGCATATCATCGT 1499 |
| 1017                                             | 1066     | 1107                                                                  | 1167<br>2352                                      | 1216<br>2412                                               | 1275<br>2472                                      | 1326<br>2532                                                                                                                        | 1386<br>2592                                                | 1446                                                       |
| Ογ<br>Dp                                         | QY<br>Dp | Qy<br>Dp                                                              | QV<br>Dp                                          | Qy<br>Db                                                   | Qy<br>Db                                          | Oy.                                                                                                                                 | o<br>S<br>S                                                 | Qy                                                         |

Search completed: May 8, 2004, 02:41:32 Job time : 5963.59 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run

7, 2004, 10:08:00 ; Search time 604.489 Seconds (without alignments) 10562.710 Million cell updates/sec May on:

US-09-303-232-5\_COPY\_95\_1597 1503 Perfect score: Title:

l atggcccctatgttggcggc.........accgcatatcatcgtgcaa 1503 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

geneseqn1980s:\*
geneseqn1990s:\*
geneseqn2000s:\*
geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\* geneseqn2003bs:\* N Geneseg 29Jan04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs:\* geneseqn2004s:\*

| SUMMARIES | Description           |          | Ab107231 |          | Ab113733 | Aaz24475 | Aac58395 | ) Aac90380 Wild-type | Aat48239 | Ada10864 | Aav44687 V274T | Aav12197 | Abs54875 Human | Abv73248 Human | Aac90385 Mutant hu | Aac90386 Mutant | Aac90387 | Abz11298 | Aat59196 | Aat59197 | Aal45873 Modified | Ab154794 | Aat59527 | 19F78660 |
|-----------|-----------------------|----------|----------|----------|----------|----------|----------|----------------------|----------|----------|----------------|----------|----------------|----------------|--------------------|-----------------|----------|----------|----------|----------|-------------------|----------|----------|----------|
| SUMMS     | E G                   | AAZ24477 | ABL07231 | AAZ24476 | ABL13733 | AAZ24475 | AAC58395 | AAC90380             | AAT48239 | ADA10864 | AAV44687       | AAV12197 | ABS54875       | ABV73248       | AAC90385           | AAC90386        | AAC90387 | ABZ11298 | AAT59196 | AAT59197 | AAL45873          | ABL54794 | AAT59527 | ADR78668 |
|           | DB                    | 3        | 4        | m        | 4        | ٣        | m        | 4                    | 7        | œ        | 7              | ~1       | 9              | 9              | 4                  | 4               | 4        | 9        | ~        | 7        | 9                 | 9        | 7        | σ        |
|           | Query<br>Match Length | 3109     | 1540     | 3700     | 936      | 2886     | 1509     | 1509                 | 1876     | 1876     | 1590           | 1876     | 1876           | 1876           | 1509               | 1509            | 1509     | 1964     | 2769     | 2101     | 1869              | 1869     | 2082     | 2752     |
| ₩         | Query                 | 100.0    | 38.3     | 38.3     | 28.6     | 27.4     | 25.1     | 24.9                 | 24.9     | 24.9     | 24.9           | 24.9     | 24.9           | 24.9           | 24.8               | 24.8            | 24.7     | 24.2     | 22.8     | 21.7     | 21.5              | 21.5     | ο.       | 20.3     |
|           | Score                 | 1503     | 575.6    | 575      | 430.6    | 411.4    | 377.2    | 374                  | 374      | 374      | 373.6          | 373.6    | 373.6          | 373.6          | 372.4              | 372.4           | 370.8    | 363.2    | 342.4    | 326.8    | 322.8             | 322.8    | 304.4    | 304.4    |
|           | Result<br>No.         | 1        | (3       | m        | 4        | Ŋ        | 9        | 7                    | 89       | 6        |                | 11       | 12             | 13             | 14                 | 15              | 16       | 17       |          | 19       | 20                | 21       | 22       | 23       |

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| 2752<br>2752<br>2752<br>2752<br>2752<br>2752<br>2753<br>3496<br>1809<br>2082<br>2082<br>2082<br>2082<br>2082                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 2277<br>2277<br>2277<br>2277<br>2664                                                                                            |
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| 44000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 1 4 4 4 4<br>2 4 5 6 4 5                                                                                                        |

## ALIGNMENTS

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds. H. virescens acetyl-choline receptor DNA from clone Hva7-2. BP. AAZ24477 standard; cDNA to mRNA; 3109 (first entry) 17-FEB-2000 AAZ24477; RESULT 1 AAZ24477 

Heliothis virescens. DE19819829-A1 11-NOV-11999

98DE-01019829. 98DE-01019829. 04-MAY-1998; 04-MAY-1998;

Adamczewski M, Oellers N, (FARE ) BAYER AG.

Schulte T;

WPI; 2000-014207/02. P-PSDB; AAY50816. New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Claim la; Page 19-22; 26pp; German.

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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neurotransmission; plant protection agent; conductance; AChR; ds
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/product= "acetyl-choline
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                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher ewkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 2.5e-149;
0; Mismatches 460;
                                                                                                                                                                                                                                                                                                                                                                                                                              Schulte T;
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64.6%;
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Best Local Similarity 64.6
Matches 929; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-014207/02.
P-PSDB; AAY50815.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499 AGCIGGACATATGACGGCAATCAGIIGGAICTGGIGCIAAAAGAIGAGGCAGGCGGCGAI
                                                                                   547 refrégactracsardestricastresactresastresastresassastresides
                                                                                                                                                                  CTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAAGAAC
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                                                                                                                                                                                                                                                                                                                        ACAATAACATACGCGTGCTGCCCCCGAGCCCTACGTGGACGTCACCTTCACCATCATGATA
                                                                                                                                                                                                                                                                                                                                                                                           667 GAAAICTACIATAATIGCIGCCGGAACCTIATAITGACATACATICGCCATTTIGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       727 AGCCCCAAAACGTIGIACTATTTTTTTCAATCTGATTGTGCCGTGCGTACTGATCGCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D. melanogaster acetyl-choline receptor DNA from clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rccardcagraccacracradara 935
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insects, used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FARB ) BAYER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the prince of specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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(also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of [II]. This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster
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                                                                                                                                                                              Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 U; 0 Other;
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Pred. No. 8.8e-104;
0; Mismatches 256;
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO10130, PRO919, PRO910105, PRO10103, PRO10137,                                                                                                                                                                                tumour; diagnosis; neoplastic disease; neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO polypeptides, useful in the of cancer.
                                                                                                                                                                                                                                              immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.
                                                                                                                                                                                                       proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney AL,
                                                                                                                                 Human PRO2145 nucleotide sequence SEQ ID NO:76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thirty PRO polynucleotides encoding treatment, diagnosis and prevention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US012252.
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99US-0145698P.
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2000WO-US000219,
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Wood WI;
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Watanabe CK,
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                                                                             Gaps
                                                                         24;
       Length 1509;
                                                                             Indels
Score 377.2; DB 3;
Pred. No. 2.2e-94;
0; Mismatches 633;
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55.2%;
Query Match 25.1
Best Local Similarity 55.2
Matches 811; Conservative
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1412 1352 1472 1457 cell culture medium for treating cells and for inducing mammalian nes to conduct calcium ions, comprising specified concentrations of sodium, calcium and potassium at specified pH. The present sequence is the coding sequence for wild-type human alpha7 nicotinic acceptlcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7-brydroxytryptcamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The GATCACCAGGAAGACTATAATGATGAACACGAGGATGAGGGAGCTGGAACTGAAGGAGAG GTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTGATGATGACTTCAGACACGGCCC 1113 GAGCGCCGTGGCGCCGCCGCCGCCAGCAACGGGAACCTGCTGTACATCGGCTTCCGCGG TCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCCG 1173 ceredeacecerecacrerererecedadececedacreredesaradreresececar--e 1231 GCCTGCTCCCCCACGCACGATGAGCACCTCCTGCACGGTGGGCAACCCCCCGGAGGGGG--GGGTAGCCACCATCGCGAGCTGCACCTCATACTGAGAGGTGCAGTTCATCACGGCCAG ------Accegactrescendarceresaciacies de la consecue del la consecue de la consecu 1338 CTTCCGCTGCCAGGACGAAAGCGAGGCGGTCTGCAGCGAGTGGAAGTTCGCCGCCTGTGT TGTTGATAGGTTTTGCCTGTTCGTGTTCACACTTTTCACAATCATCGCGACAGTAGCTGT 1353 GATGAAGAAGCTGATGAGGAAGCCGAGCTGATCAGCGACTGGAAGTTTGCTGCGATGGT 1398 GGTGGACCGCCTGTGCCTCATGGCCTTCTCGGTCTTCACCATCATCTGCACCATCGGCAT Human; alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss. Wild-type human alpha7 ligand gated ion channel coding

1352

1230

1412

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Nucleic acids encoding nicotinic acetyl:choline receptor sub-units - used
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                                                                                                                                1053 GATCACCAGGAAGACTATAATGATGAACACGAGGATGAGGGAGCTGGAACTGAAGGAGAG
                                                                                                                                                                                GTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTGATGATGACTTCAGACACGGCCC
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ligand-gated receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuronal nicotinic acetylcholine receptor alpha-7 subunit DNA
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alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells
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                                                                                                      Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;
                                                                                                                                                     Score 374; DB 4; Length 1509
Pred. No. 1.7e-93;
0; Mismatches 635; Indels
                                                                                                                                                     Query Match
Best Local Similarity 55.1%;
Matches 809; Conservative
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                                                                                                                 A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammallan cells or amphibitan occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48212-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs
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Pred. No. 1.9e-93;
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                                                                                                                                                                                                                                                                                                                                   Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;
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to determine the effect of drugs on
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                                                           Disclosure; Page 71-73; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cetylcholine receptor (nachs) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha? naChR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neuroageneration, ench as cancer, post-herpetic neuralgia, diabatic dysfunction, such as cancer, post-herpetic neuralgia, diabatic psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha? nachR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
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                   Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 373.6; DB 2;
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24.9%;
Best Local Similarity 55.0%;
Matches 808; Conservative 1
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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NAKChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human
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/product= "NAChR alpha7 subunit"
/note= "neuronal nicotinic acetylcholine receptor"
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Pred. No. 2.5e-93;
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                                         GTGCTGCCCCGAGCCCTACGTGGACGTCACCTTCACCATCATGATAAGAAGACGAACCTT
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Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caagaactacaarcectregagagagecegregeceaargacregeaacecacecerera
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Human; alpha7 nicotinic acetylcholine gated ion channel;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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Human, alpha7 nicotinic acetylcholine gated ion channel; mutant; 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.

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Berkenpas

Groppi VE, Wolfe ML,

2001-061524/07.

P-PSDB; AAB50016.

(PHAA ) PHARMACIA & UPJOHN CO

25-MAY-2000; 2000WO-US011862.

WO200073431-A2

07-DEC-2000.

Homo sapiens,

99US-0136174P.

27-MAY-1999;

alpha7 ligand gated ion channel

Mutant human

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                                                                                                                    CGCGTGGTTTCCCTTCGACGACCACACTGTGATATGAAGTTCGGTAGCTGGACATATGA
                                                                                                                                                                 ACGCTGGTTTCCCTTTGATGTGCACACTGCAACTGAAGTTTGGGTCCTGGTCTTACGG
                                                                                                                                                                                                                                         AACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAACACAATAACATACGC
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CGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACATGCAAGATGGACAT
                                     TICTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAAGAGTTCCTGCTACATGT
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1458 CCTGATGTCGGCTCCCAACTTCGTGGAG 1485 7, 2004, 15:01:54 셤

Search completed: May 7

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GenCore version 5.1.6
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using sw model OM nucleic - nucleic search,

May on:

7, 2004, 14:08:32; Search time 4039.19 Seconds (without alignments) 11111.850 Million cell updates/sec

US-09-303-232-5\_COPY\_95\_1597

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IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

27513289 seqs, 14931090276 residues

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

ESI: \*

Database

em\_estba:\*
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em\_gss\_pbg:\*
em\_gss\_vrl:\*
gb\_gssl:\* em\_gss\_pln:\*
em\_gss\_vrt:\*
em\_gss\_fun:\*
em\_gss\_mam:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |   |        | Description        |        | BG632919 GH16126.3 | AI292581 GH15518.5 | CD013901 90134548 | AL530299 AL530299 |
|-----------|---|--------|--------------------|--------|--------------------|--------------------|-------------------|-------------------|
| SUMMARIES |   |        | ΩI                 |        | 12 BG632919        | AI292581           | 14 CD013901       | AL530299          |
|           |   |        | DB                 | i      | 12                 | σ                  | 14                | δ                 |
|           |   |        | Match Length DB ID | 111111 | 885                | 607                | 2296              |                   |
|           | æ | Query  |                    | 1      | 28.2               | 22.0               | 20.1              | 20.0              |
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|----------------------|-----------------------------------------|---------------------------------------------------------------------------------|---------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------|-----------------------------------------------------|
| 3422<br>3422<br>3315 | 224 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | AY402876<br>AY402875<br>AY402877<br>AK080475<br>CB245337<br>AY406232<br>AX06232 | 3885<br>3885<br>3885<br>3885<br>780<br>780                                      | AY40'186<br>CD804155<br>CF742344<br>CB149460<br>AY406231<br>AX033068<br>AY411329<br>AY411329<br>CF530720 | 0312<br>1420<br>11171<br>2695<br>3818<br>3982       |
| 29<br>11<br>29       | наннан                                  | 00014001                                                                        | 13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>1 | 2                                                                                                        | 11111111111111111111111111111111111111              |
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| 9999                 |                                         | 18.3<br>17.2<br>17.2<br>16.8<br>16.8                                            |                                                                                 | <b>uuuuuu444</b>                                                                                         |                                                     |
| 94.<br>93.<br>86.    |                                         | 74.<br>72.<br>72.<br>56.<br>56.                                                 | <del></del>                                                                     | 10 20 30 20 10 10 10 10 10 10 10 10 10 10 10 10 10                                                       |                                                     |
| 12 6 7 6 51          | 111<br>111<br>122<br>141<br>141         | 15<br>17<br>18<br>19<br>20<br>20                                                | E 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                         | 2                                                                                                        | 6 4 4 4 4 4 6 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 |
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## ALIGNMENTS

BG632919
GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Based upon the presence of a XhoI site followed by a run of 14 or Unpublished (2001) Other ESTs: GH16126.5prime Contact: Stapleton, M. BG632919.1 GI:13758409 EST. ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BG632919/c LOCUS DEFINITION TITLE JOURNAL COMMENT REFERENCE AUTHORS

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941 TACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI292581
607 bp mRNA linear EST 02-DEC-2003 GH15518.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cone GH15518 5 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. AI292581
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Xho1; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rerirerecrericarerireidecearaarraaagaagerereaagacerereaaa 134
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104 İCCİCAATIATCATCATAGAAATCCAGATACGCATGAATGAGTGAATGGGTAATAGTTT 45
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                                     164 GAACTTATTTCAATTGCATTATGTTTATGGTGGCCTCATCAGTTGTTGTCAACCATACTTG
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
htt genomic AE003626: arm:2L [9617316,9882551]
estimated-cytc:30C7-30F4: 04/10/2001
Plate: GH:155 row: B column: 6
High quality sequence stop: 521
POLYA=No.
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Pred. No. 3.1e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Other ESTs: GH15518.3prime
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI292581.1 GI:3941988
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   more T residues at the beginning of the sequence, polyadenylated. The resulting Poly-T sequence has genomic AE003511: arm:X [18792641,19136447] estimated-cyto:18A3-18C6: 04/10/2001 Plate: GH.161 row. C column: 2 High quality sequence stop: 784. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 423.8; DB 12; Length
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2296)

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/note="Wector: pDrive Cloning Vector; RT-PCR was perforusing gene-specific primers flanking the open-reading trame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and
                                                                                                                                                                                   AATCGGAGCCCCTGGAGGTTAAGTTCGGACTGACGCTGCAGCAGATCATCGACGTGGACG
                                                                                                   AGAAGAATCAGCTTCTCATAACGAATCTTTGGCTTTCGTTGGAGTGGAACGACTACAATC
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                                                  <u> AGAAGAATCAACTTATAACCAATATATGGCTGTCGTTGGAGTGGAATGACTACAACC</u>
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Pred. No. 1.2e-64;
0; Mismatches 433; Indels 3;
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Unpublished (2003)

Contact: Jin, P.

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160 Porter Drive, Palo Alto, CA 94304,

Tel: 650 621 8639

Fax: 650 621 8965
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PCR isolation and cloning of novel spli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       968 GATCATGCCCGCAACATCCGATTCGGTACCATTGAWAGCCCAGTTCTTCGCCCAGCACCAT 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GAGAAGAGTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTGGCC 126
                                                                                                                                                                                                                                                                                                                                                                                            TGCTGATCTCATCGATGGCACTCCTCGGCTTCACACTGCCACAGACTCCGGAG--AGAA 782
                                                                                                                                                                                                                                                                                                     TCACAGTGACCATGCGCCGCAGGACGCTCTACTATGGCCTCAACCTGCTGATCCCCTGTG 847
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, B., Fu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                אות 1436 bp DNA linear GSS 15-DEC-:
Homo sapiens CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                       728 ccescialege de la contra de la contra de la contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1028 GATCATCGT-GGGCTTTGGGTTGKKRMGGTGATCGTGCTGCAGTACCAC 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTCATGGTAGCGTCGTCTGTGGTACTGACTGTGGTGGTACTCAATTACCAC 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              э;
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Pred. No. 7e-63;
0; Mismatches 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2003) Celera Genomics,
Rockville, MD 20850, USA
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CHRNA3"
/locus_tag="HCM1369"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:39758856
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57.1%;
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AUTHORS
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JOURNAL
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AY402873
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mol_type="mRNA"
/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="CSODDOO7YPO5"
/tissue type="NEUROBLASTOWA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                       On Feb 13, 2001 this sequence version replaced gi:12793792.
Contact: Genoscope
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BP 191 91006 EVRY cedax - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgiban/Coluster.gi?seq=CS0DD007CH03QPl&cluster=7646.r. Contact :
                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODD007CH03QP1.
Location/Qualifiers
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I (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Lil, H.B., Gruber, C., Jessee, J. and normalization
Unpublished (2001)
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Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus.

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                              Chordata; Rodentia;
                                     HTC; CAP trapper.
Mus musculus (house mouse)
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Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Ohsato, M., Okazaki, Y., Saito, R., Saito, H., Sakai, K., Shinagawa, A., Shiraki, T., Sanio, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, H., Tanaka, T., Tasanishi, A., Tayanishi, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Pargloration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDRAs

Nature 420, 563-573 (2002)

6 (bases I to 2940)
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Fax:81-45-503-9216)
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HTC 18-SEP-2003

Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.

mRNA

2940 bp

AK034228

DEFINITION

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Sciurognathi, Muridae; Murinae; Mus.
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Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone: C630019M18 product: cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria;
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/brotein_id="BAC28638.1"
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DPGDYENVTSTRIPSELIWRPDIVLYNNANGGGFRATHLFYDRAVGWTPPRAIYK
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EPGTLIGDICNGGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSSVEKASPCPSPG
SCHPPNSGAPVLIKARSLEVGHVPSSQEAAEGESIRCRSKSTQVCVSQAASLTESK
PTGSPASLKTRPSQLPVSDQTSPCKCTCRESPVSPITTAKAGGTKAPPQHLPLSPAL
TRAVECVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLMMFIIVCLLGTVGLELPPAL
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TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLNFYENGER
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nicotinic, alpha polypeptide 4 (MGD|MG1:87888,
GB|NM_015730, evidence: BLASTN, 99%, match=1946)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="diencephalon"
/clone_lib="RIKEN full-length enriched
/dev_stage="adult"
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Pred. No. 2.5e-62;
0; Mismatches 453;
                                                                                                                                                                                                                                                                    /db_xref="FANTOM_DB:9330165116"
/db_xref="MGI:2398424"
URL:http://fantom.gsc.riken.go.jp/
                                                                                                                             'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                         /db_xref="MGI:2398424"
/db_xref="taxon:10090"
/clone="9330165116"
                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
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DPGDYENVTSIRIPSELIWRPDIVLYNNADGDFAVTHLTKAHLFYDGRYQWTPPAIYK
SSCSIDVTFPFDQQNCTWKFGSWTYDKAKIDLVSMHSRVDQLDFWESGEWVIVDAVG
TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSECGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MEIGGSGAPPPLLLLPLLLLGTGLLPASSHIETRAHAEERLLK
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'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                on functional annotation
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             Kawai, J
                                                                                                                                                                        RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Rike
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                 FANTOM Consortium and the RIKEN Genome Exploration Research
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai OkazaKi,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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GB|NM_015730, evidence: BLASTN, 99%, match=1946)
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(MGD|MGI:87888,
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                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome based of 66,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="FANTOM_DB:C630019M18"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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PTGSPASLKTRRSQLFVSDQTSPCKCTCKEBSPVSPITVLKAGGGTKAPPQHLBLSPAL
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| 307 AAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACC 366 261 NNNNCTGGAAGCCNACATTGTGTGTTGTGTATAATAGTGCTGACGGGATTTTTGACGGGACC 320 367 TACCAGACCAACGTGGTGGTCACAAGCGGCGGCGAGTTGCTGTACGTGCCACCTGGAC 320 321 GAAGACCAACGTGGTGGTACACAGAAGAGACGAGTTGCTTACGTACG                                                                               | 487 ATGAAGTTCGGTAGCTGGACATATGACGGCAATCGGTCTGGTGCTAAAAGATGG 546 411 ATGAAGTTCGGTAGCTCGGTCTACGGTAAAAGACGAAATCGATCTGGTCTGAT— 411                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | AKO81254 AKO81254 AKO81254 AKO81254 DIOCUS MAS musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030030P04 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence. AKO81254.1 GI:26099790 AKO81254.1 GI:26099790 HTC; CAP trapper. AKO81254.1 GI:26099790 HTC; CAP trapper. Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) Mus musculus (house mouse) ACHGNES ORGANISM Mus musculus (house mouse) AUTHORS CALINICA, Pand Hayashizaki, Y. High-efficiency full-length cDNA cloning JOURNAL Meth. Enzymol. 303, 19-44 (1999) PUBMED 10349636                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| Oy 911 TAGCGTCGTCTGTGGTACTGTGGTGGTACTCAATTACCACCATCGAACAGCTGATA 970  Db 991 TCACCCTCTCCATTGTCATCACGGTCTTCGTGCTCAATGTACCACCGCTCACCACGCA 1050  Qy 971 TACATGAAATGCCACAGTGGATAAAATCCGTATTCCTACATGGTTGCTGCTTGC 1030  Db 1051 CACACACCATGCCGCTGGGTGCGCAAGTCTTCCTGGACATTGTGCCCGTCTCCTCT 1110  Qy 1031 GAATGTCGAGGCCA 1044  Db 1111 TCATGAAAGCGCCA 1124 | RESULT 8 AY402874 LOCUES LOCUES AY402874 AY402874 AY402874 LOCUES DEFINITION Pan troglodytes CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence, ACCESSION AY402874. GI:39758857 SURVENCE SOURCE Pan troglodytes (chimpanzee) Pan troglodytes (chimpanzee) Pan troglodytes (chimpanzee) Pan troglodytes CLATKA.G., Glanoweki.S., Nielson.R., Thomas.P., Kejariwal,A., TARACHARAN.A., Tanenbaum.D., Civello,D.R., Lu,F., Murphy,B., AUTHORS TITLE AUTHORS TITLE TOGALM.A., Tanenbaum.D.M., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M., Civello,D.R., Thomas.P., Kejariwal,A., TITLE TOGALM.A., Tanenbaum.D., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M., Civello,D.R., Lu,F., Murphy,B., TOGA,M.A., Tanenbaum.D., Civello,D.R., Lu,F., Shinsky,J.J., Adams,M.D. and Cargill,M., Civello,D.R., Lu,F., Shinsky,J.J., Adams,M.D. and Cargill,M., This sequence was made by sequencing genomic exons and ordering them based on alignment.  FEATURES  1. 1436  ADDITIONAL SUMMISSIEM.PAN ENDER TORDANAL SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER TORDANAL SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER TORDANAL SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER TORDANAL SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER TORDANAL SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN ENDER SOURCE  ADDITIONAL SUMMISSIEM.PAN EN | Query Match Best Local Similarity 55.6%; Pred. No. 7.38-61; Matches 544; Conservative 0; Mismatches 431; Indels 3; Gaps 1; Matches 544; Conservative 0; Mismatches 431; Indels 3; Gaps 1; Oy 67 GAGAAGACATCCTGCAACGCTTGCTGCAACCCTGCAGCGCACCGTGGCC 126 Db 21 GAGCACCGTTATTGAGCGGTTTTGAACATTACAACACACTGCGCCTGGCC 80  Cy 127 AACGAGACCGCAACGCTATTTATACCATTTACACTGCAAATCATTGACGTG 186 Db 81 AACGTGTTCACTTATTATACCATTTANNGGTGCATGCTTGCAAATCATTGAAGGTG 140  Oy 187 GACGAGAGAATCAACTACTTATAAACCAATATTGGCTGTTGGAGTGGAATGACTAC 246 Db 141 GATGAAGTAAACACACTACTTATAAACCAAATATGGCTGTTGGAAATGACTAC 200  Oy 247 AACCTGAAGTGGAACGAACTACTATGAGGGGGTCAAGGAAATCTACCAAGGTGCTAAGGAATGACTAC 200  Oy 247 AACCTGAAGTGGAACCGAGTATGGGGGGGGTCAAGGAAATCTACGCCCAAC 306 Db 201 AAGCTGAAGTGGAACCCACTATGATGTGGGGGGGCAAAGGAACCTCAGGATCATGCAAAGACCAACACTATGAGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |

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218 445 278 338 565 398 625 458 685 518 745 578 802 638 860 869

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/note="cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891, GB|NM_009602, evidence: BLASIN, 99%, match=1498)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1154 TGTGCTCAATGTGCACCACCGTTGGCCTACCACGCACACCATGGCGCCCTGGGTCAAGGT 1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1094 GGGAAAGTACCTCATGTTCACCATGGTGCTAGTCACCTTCTCCATCGTCACTAGCGTGTG 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         939 GGTACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATC 998
                                                                                                                                                                                                                                                                                                                                                                  CTACAACACCCTGGAGCGACCGGTGGCCAACGAGGGGGAACCGCTAGAGGTCAGGTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                CTATAACAAGCTGATCCGTCCAGCTACTAATGGCTCTGAGCTGGTGACTGTACAGCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 CTTGACCTTGCAGCAAATCATTGACGTGGACGAGAAATCAACTACTTATAACCAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 ATGGCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACAGCGAGTATGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 GGTCAAGGACCTCAGGATCACGCCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 CAATGCTGACGCCATGTACGAAGTCTCCTTCTATTCCAATGCTGTGGTCTCCTATGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 CAGTIGCCTGTACGIGCCACCTGGCATATICAAGAGCACATGCAAGAIGGACATTGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        626 CAGCATCTTTTGGCTACCGCCTGCCATCTACAAGAGCGCATGCAAGATTGAGGTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 GTTTCCCTTCGACGACCAACACTGTGATATGAAGTTCGGTAGCTGGACATATGACGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686 CTTCCCATTTGACCAGCAGAACTGCACCATGAAGTTCCGCTCCTGGACCTACGACCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            519 TCAGTTGGATCTGGTGCTAAAAGATGAGGCAGCGGCGATCTATCGGACTTCATAACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746 TGAGATTGACCTGGTGCTCAAAAGCGATGTGGCCAGC---CTGGACGACTTCACACTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 GGTATCATTGGCACAGCTCATCAGTGTGCACGAGCGGAGCAGATCATGACCACCAACGT
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                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                        Score 281.6; DB 11;
Pred. No. 2.3e-59;
0; Mismatches 389;
                         dev stage="adult"
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Local Similarity 57.7%;
les 547; Conservative
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
                                                                                                                                                                                                                                                                                        Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Zakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, X., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKBN integrated sequence analysis (RISA) system--384-format genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details
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/clone="C030030P04"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
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SFYPDIQUATYDFTSHTEIDLVLKSDVVSLDDFTPSGEWDIALPRPDD
SFYPDITYDFTIRREFFYTINLIPCVLTTSLAILVFYLESGEWTICTSVLLAL
TVFLLLISKIVPFTSLDVFLVGKYLMFTMVLVTFSIVTSSVCVLNVHHRSPTTHTMAPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKVVFLEKLPTLLFLOOPRHRCARORLRLRRROREREGAGTLFFREGPAADPCTCFVN
PASMOGLAGAFQAEPAAAGLGRSMGPCSCGLREAVDGVRFIADHMRSEDDDOSVREDW
KYVAMVIDRLFLWIFVFVCVFGTIGMFLOPLFONYTATTFLHSDHSAPSSK"
                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to pivision of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://fantom.gsc.riken.go.jp/.

Location/Qualifiers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 CTTGACCTTGCAGCAAATCATTGACGTGGACGAGAAGAATCAACTACTTATAACCAATAT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCAAGGACCTCAGGATCACGCCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAA 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product; cholinergic receptor,
nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASIN, 99%, match=1498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACAACACCCTGGAGGGACCGGTGGCCAACGAGAGCGAACCGCTAGAGGTCAGGTTCGG
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="FANTOM DB:C530044P16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="spinal cord"
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/dev_stage="12 days embryo"
200. 1705
                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/clone="C530044P16"
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Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length CDNAs

L Mature 420, 563-573 (2002)

E ( bases 1 to 4037)

6 (bases 1 to 4037)

7 Adachi,J., Alarawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Haramato,K., Haraka,T., Hirozane,T., Hayashida,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katch,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kosukawa,T., Koya,S., Kurihara,C., Mateuyama,T., Miyazaki,R., Murata,M., Koya,S., Kurihara,C., Mateuyama,T., Miyazaki,R., Murata,M., Ohsato,N., Okaamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Santo,R., Saito,R., Saitoh,H., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Murata,M., Mataka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                                                                                                                               Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530044P16 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
AKO49722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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1214 GGTCTTCCTGGAGAAGCTGCCCACCTTCCTTCCTGCAGCAGCCACG 1261
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Direct Submission
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Direct Submission
Submitted (16-JUL-2011) Yoshihide Hayashizaki, The Institute of Ephysical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-res@gsc.riken.go.]p, WIR:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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KKVRLPSKHIWLPDVVLYNNADGMYEVSFYSNAVVSYDGSIFWLPPAIYKSACKIEVK
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STYVDITYDFIIRRKPLFYTINLIIPCVLITSLAILVFYLPSDCGEKMTLCISVLLAL
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VKVVFLEKLPTLLFLQQPRHRCARQRLRLRRRQREREGAGTLFFREGPAADPCTCFVN
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KYVAMVIDRLFLMIFVFVCVFGTIGMFLQPLFQNYTATTFLHSDHSAPSSK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               יראסים בוגם="גוגאבו full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
209. יחוא
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                               Team and the
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nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASIN, 99%, match=1498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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/clone_lib="RIKEN full-length
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/protein_id="BAC34749.1"
/db_xref="GI:26342174"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
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6 (bases 1 to 4046)
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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:10100/70121 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
         TCAGTTGGATCTGGTGCTAAAAGATGAGGCAGGCGGCGATCTATCGGACTTCATAACAAA
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High-efficiency full-length cDNA cloning
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The Favior Color of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

In Nature 420, 563-573 (2002)

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S Adachi, J. Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Haramoto, K., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Haraka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kojima, Y., Kondo, S., Komno, H., Kasukawa, T., Kojima, Y., Minazaki, A., Murata, M., Kojima, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Saitok, S., Shibata, K., Shibata, K., Shibata, R., Shibata, R., Shibata, R., Shibata, R., Shibata, R., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomatu, A., Toya, T., Yasunishi, A., Takada, Y., Tanaka, T., Tomatu, A., Toya, T., Yasunishi, A.,
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALFHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Fax:81-45-503-9216)
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High-efficiency full-length cDNA
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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130068A06 product:NEURONAL NICOTINIC AKCETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.

AKO51730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1011 GATTTTTGTCACCTTGTCCATCGTCATCAGTCTTTGTGCTCAACGTGCACTACAGAAC 1070
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Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                 TGATATGAAGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTGCTAAAAGA
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein id="BAC35404.1"
|db_xref="C1:26343495"
|/translation="MGVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFEDYNEII
|RPVANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLMLKQIWNDYKLKMKRESDYQGVEF
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                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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         to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGCCGCTGTCCATGCTGATGCTGTGTGTGCTGCTGCCAGTGGCCAGGGCCTCGGA
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Division of Experimental Animal Research in Riken contributed prepare mouse tissues.
Please visit our web site for further details.
URL:http://fancome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Pred. No. 5.5e-58;
0; Mismatches 469; Indels
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/db_xref="MGI:2425288"
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94. .1593
                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                             xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                            /clone="E130103E14"
                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
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/translation="WOVVLEPPLSMLMLVLMLLPVASASEAEHRLFOYLFEDYNBII

RPVANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWKPSDYQSVEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA library"
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsuunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, X., Kira, A. and Hayashizaki, Y. RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 2916)
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/clone_lib="RIKEN full-length enriched 'dev stage="12 days embryo"
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730007914 product:NEURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                  ĠAŤTTŤTĠŤCAĊĊŤTĠŤĊOŤĊĠŤĊAŤĊĀĊĀĠŤĊŢŤŦĠŤĠĊŤĊĂĠĠĠĊŦĀĊĀĠĀĠ 1146
                                                                                                                                                                               963 AGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCATG 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inouce, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer cenalysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
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Analysis of the mouse transcriptome based on functional annotation Nature 420, 563-573 (2002)

( (bases 1 to 3126)
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Rodentia, Sciurognathi, Muridae, Murinae; Mus.
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                                          1027 GACCATCCTTCCACCTCACTGTCATCCCTTGATCGGGGGGAGTACTCTCTTCACTAT
                                                                                       903 GITCAIGGIAGCGICGICTGIGGIACIGACIGIGGIACICAAITACCACCAICGAAC
GACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCAT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
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Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nahi, K., Namazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sagabe, T., Tagami, M., Tagawa, A., Shinagawa, A., Shiraki, T., Sogabe, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Towaru, A., Toya, T., Yasunishi, A., Direct Submission and Hayashizaki, Y. Toya, T., Yasunishi, A., Direct Submission and Hayashizaki, Y. Direct Submission and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, REX:81-45-503-9212,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNEIIRPVAAVSHPVIIQFEYSMSQLVKVDEVNQIMETNIMLKQIWNDYKLKÄKRESDY
QGVEFMRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKI
DVIYFPFDYQNCTMKFGSWSYDKAKIDLVIIGSSMNLKDYMESGEWAIIKAFF
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HYMPYWKAVPLNLLPRVMFWTRPTSTSEDAPKTRNFYGABLSNLNVFSRADGSKSCKE
GYPCODGTGGYCHHRYNKI SNFSANLTRSSSSBSVDAVLSLSALSPEIKBAIGSKSCKE
AENMKAQNVAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGIBLQPLMARDDT"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MRSSDMGVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFED"
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URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Pred. No. 7.2e-58;
0; Mismatches 469;
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/protein_id="BAC37909.1"
/db_xref="G1:26348539"
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| db xref="MGI:2407635"
| db xref="taxon:10090"
| clone="A730007P14"
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/strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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GI:39758859

AY402876.1 GSS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION RESULT 15 AY402876

Homo sapiens (human) Homo sapiens

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                          1 (bases 1 to 1442)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbam, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                              Clark, A.G., Glancwski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glancwski, S., Nielson, R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Admas, M.D. and Cargill, M.

Direct Submitsion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Selexa Genomics, 45 West Gude Drive, Submitted was made by sequencing genomic exons and ordering them based on alignment.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 9.8e-58;
0; Mismatches 401;
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/organism="Homo sapiens'
/mol type="genomic DNA"
/db_xref="taxon:9606"
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/gene="CHRNB4"
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Best Local Similarity 57.0%;
Matches 547; Conservative (
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951 TGCTTCCTGCACAAGCTGCCTACCTTCCTCATGAAGCGCCCTGGCCCCGACAGCAGC 1010
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771 ITCTICETGCTGCTGTCTCGAGATCGTGCCACCCCCCCCGATGTGCCTCTCTAIC 830
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Compugen Ltd.
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Copyright (c) 1993 - 2004
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US-09-303-232-6 2640 1 MAPMLAALALLALLPVSEQG......LFTIIATVAVLLSAPHIIVQ 501 Title: Perfect score: Sequence:

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A Geneseq 29Jan04:\* geneseqp1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMADTES

|           | scription     | Aay50816 H. viresc | 5 H.     | Ω.       | Dro      | m        | m        | Aaw09025 Neuronal | Aab24088 Human PRO | Aab82690 Nicotinic | N        | Abg70492 Human neu | Abb82435 Human neu |          | 1 Human  | 0 Human  | 6 V274T  | Aaw12368 Neuronal | Aab50015 Mutant hu | Aab50016 Mutant hu | Ade57308 Rat Prote | Add47049 Rat Prote | Aab50017 Mutant hu | 6        | 4        | Abp96318 Caenorhab |
|-----------|---------------|--------------------|----------|----------|----------|----------|----------|-------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|----------|----------|----------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|
| SUMMAKIES | ΩI            | AAY50816           | AAY50815 | AAY50814 | ABB60432 | ABB63683 | AAW44153 | AAW09025          | AAB24088           | AAB82690           | AAB50012 | ABG70492           | ABB82435           | ADA10874 | ADD47051 | ADE57310 | AAW69216 | AAW12368          | AAB50015           | AAB50016           | ADE57308           | ADD47049           | AAB50017           | AAW12369 | AAE12824 | ABP96318           |
|           | DB            | 3                  | т        | m        | 4        | 4        | 7        | 7                 | m                  | 4                  | 4        | 2                  | Ŋ                  | 7        | 7        | 7        | 7        | 7                 | 4                  | 4                  | 7                  | 7                  | 4                  | ~        | 4        | 9                  |
|           | Length        | 501                | 496      | 770      | 498      | 311      | 502      | 205               | 502                | 502                | 502      | 502                | 502                | 502      | 502      | 502      | 502      | 502               | 502                | 502                | 502                | 502                | 502                | 511      | 554      | 554                |
| ф         | Query         | 100.0              | 68.3     | 6.09     | 59.5     | 48.6     | 47.7     | 47.7              | 47.7               | 47.7               | 47.7     | 47.7               | 47.7               | 47.7     | 47.7     | 47.7     | 47.5     | 47.5              | 47.4               | 47.3               | 47.2               |                    | 47.1               | 46.5     | 40.9     | 40.9               |
|           | Score         | 2640               | 1803.5   | 1609     | 1570.5   | 1283     |          | 1258.5            | 1258.5             | 1258.5             | 1258.5   | 1258.5             | 1258.5             | 1258.5   | 1258.5   | 1258.5   | 1254.5   | 1253              | 1252.5             | 1248.5             | 1246.5             | 1246.5             | 1242.5             | 1226.5   | 8        | 1080               |
|           | Result<br>No. |                    | 7        | e        | 4        | 5        | 9        | 7                 | <b>c</b> o         | თ                  | 10       | 11                 | 12                 | 13       | 14       | 15       | 16       | 17                | 18                 | 19                 | 20                 | 21                 | 22                 | 23       | 24       | 25                 |

| Ade57314 Human Pro | Ade57318 Human Pro | Aaw09022 Neuronal | Adal0857 Human neu | Ada83810 Human CHR | Ade57312 Rat Prote | Ade57316 Rat Prote | Aab50014 Chimeric | Abg70488 Human neu | Abb82431 Human neu | Abb61954 Drosophil | Aab50018 Mature ce | Aaw44156 Human neu | Aaw09018 Neuronal | Abg70491 Human neu | Abb82434 Human neu | Adal0863 Human neu | Abb62727 Drosophil | Aaw44155 Human neu | Aar73966 Alpha 2 s |
|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ADE57314           | ADE57318           | AAW09022          | ADA10857           | ADA83810           | ADE57312           | ADE57316           | AAB50014          | ABG70488           | ABB82431           | ABB61954           | AAB50018           | AAW44156           | AAW09018          | ABG70491           | ABB82434           | ADA10863           | ABB62727           | AAW44155           | AAR73966           |
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| 503                | 503                | 504               | 504                | 502                | 499                | 499                | 470               | 504                | 504                | 576                | 448                | 504                | 494               | 494                | 494                | 494                | 580                | 529                | 529                |
| 37.5               | 37.5               | 37.5              | 37.5               | 37.2               | 37.0               | 37.0               | 36.5              | 35.9               | 35.9               | 35.7               | 35.7               | 35.6               | 35.3              | 35.3               | 35.3               | 35.3               | 35.3               | 34.9               | 34.9               |
| 989.5              | 989.5              | 989.5             | 989.5              | 982.5              | 977.5              | 977.5              | 962.5             | 946.5              | 946.5              | 943                | 942                | 940.5              | 933               | 933                | 933                | 933                | 933                | 922.5              | 922.5              |
| 26                 | 27                 | 28                | 29                 | 30                 | 31                 | 32                 | 33                | 34                 | 35                 | 36                 | 37                 | 38                 | 39                | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR. H. virescens acetyl-choline receptor protein from clone Hva7-2. AAY50816 standard; protein; 501 AA. (first entry) 17-FEB-2000 AAY50816; AAY50816
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98DE-01019829. Heliothis virescens DE19819829-A1 04-MAY-1998; 11-NOV-1999.

(FARB ) BAYER AG.

98DE-01019829.

04-MAY-1998;

Adamczewski M, Oellers N,

Ė

Schulte

WPI; 2000-014207/02.

N-PSDB; AAZ24477

New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Example 1a; Page 22-23; 26pp; German

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens

Sequence 501 AA;

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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (III). This sequence represents an acetylcholine receptor isolated from Heliothus virescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STYPINVVVRNIGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 APMLAALALLALLPVSEQ-GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRTLYYFFNLIVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 PPPPDLELRERSSKSLLANVLDIDDDFRH-----PQAQQ------PQCCRY---YRGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 PSTMEDVGGGLGSH-----HRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRF
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D. melanogaster acetyl-choline receptor protein from clone Da7
                                                                                                                                                                                                                                                                                                                                  68.3%; Score 1803.5; DB 3; Lenyc...
68.7%; Pred. No. 8.2e-180;
... wi.mmarches 78; Indels
insects, used to identify potential insecticides.
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                                      Example 1a; Page 17-19; 26pp; German.
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                                                                                                                                                                                                                                                                                                                                                  Query Match 68.3°
Best Local Similarity 68.7°
Matches 347; Conservative
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                                                                                                                                                                                                                                                                                                                                DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP 240
                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420
                                                                                                                                                                          DVDEKNQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD 120
                                                                                                                                                                                                                                                       GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MFMVASSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMN 360
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                                                                                                                                                                                                DVDEKNOLLITNIMLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFD
                                                                                                                     MAPMLAALALLALLPVSEQGPHEKRLLINALLANYNTLERPVANESBPLEVRFGLTLQQII
                                                                                                                                                                                                                                                                               GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK
                                                                                                                                                                                                                                                                                                                                                                      DEAGGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                             CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSTMEDVGGGLGSHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRFCLFVF
                                                                                               1 MAPMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQ11
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid encoding a nicotinic acetylcholine receptor from
                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H. virescens acetyl-choline receptor protein from clone Hva7-1
                  Length 501;
                                                        Indels
                    Score 2640; DB 3;
Pred. No. 1.2e-267;
                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schulte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLFTIIATVAVLLSAPHIIVQ 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY50815 standard; protein; 496
                      100.08;
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                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                  Query Match
Best Local Similarity 100.
Matches 501; Conservative
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N-PSDB; AAZ24476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARB ) BAYER AG.
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DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV
                                                                     ABB60432 standard; protein; 498
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                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-0191637P
                                                                                                                                                                                                                                                                                                                                                            2000US-00614150
                                                                                                                             (first entry)
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                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB: ABL04535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 498 AA;
                                                                                                                                                                                                    pharmaceutical
                                                                                                                                                                                                                                                          WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                              11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nteractions.
                                                                                                                             26-MAR-2002
                                                                                                                                                                                      Drosophila;
                                                                                                                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC,
725
                                                                                                  ABB60432
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Matches
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                                                                                                                                                                                                                                                                                             This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLIS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMALLGFTLPPDSGEKLTLGVTLLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRK---TIMMNTR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------MRELELKERSSKSLLANVLDIDDFRHG--PPPPNSTASTGNLGPGCSIFRTD 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618 SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRFWTPG-----GTLPHNPAFYRTV 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ELHLILRELQFITARMKKA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LLALLPVSEQ----GPHEKRILNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 NQLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                          New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 DEEAELISDWKFAAMVDRFCLFVFTLFTIIATVAVLLSAPHIIV 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1609; DB 3;
; Pred. No. 4.2e-159;
57; Mismatches 65;
                                                                                                                                                      Schulte T;
                                                                                                                                                                                                                                                                      Example 1a; Page 12-14; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 FRRSFVRPSTMEDVG--GGLGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.9%;
                                                                  98DE-01019829
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Best Local Similarity 60.83
Matches 319; Conservative
                                                                                                                                                        Oellers
                                                                                                                                                                                   2000-014207/02.
                                                                                                                                                                                               N-PSDB; AAZ24475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 770 AA;
                                                                                                                                                      Adamczewski M,
         DE19819829-A1
                                                                                                                          (FARB ) BAYER
                                                                  04-MAY-1998;
                                                                                             04-MAY-1998;
                                    11-NOV-1999
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63 LQQIIDVDEKNQILTINAWLNLEWNDYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                   developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.5%; Score 1570.5; DB 4; Length 498; llarity 61.1%; Pred. No. 2.4e-155; Conservative 44; Mismatches 84; Indels 75;
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                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 8088
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30; Mismatches
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  231; Conservative
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  266
                                                                                                                 292 ADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQC-RAESTYFNCIMFMVASSVVLTV 350
                                                                                                                                                                                                                                                                      SKSLLANVLDIDDDFRH-----TISGSQTAIGSS-----ASFGRPTTVEEHHTAIG 456
                                    --ILFFQFNCAMCANLIDGPTGLHIAAĞFGRETDAĞRNYTTIINSISKPCRRVH 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABL16176) and the encoded proteins (ABBS7737-ABR37272). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                            TILLSLTVFLNLVABTLPQVSDAIPLLGTYFNCIMFMVASSVVLTV
                                                                                                                                                       WYLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMRELELKERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English.
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  ----GFTLPPDSGEKLTLGV-
                                                                                                                                                                                                                                                                                                                                   CNEKDLHLILKELOFITARMRKADDEAELIGDWKFAAMVVDR 498
                                                                                                                                                                                                                                                                                                               SHHRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDR 474
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Pred. No. 1.8e-125;
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  FTIMIRRRILYYFFNLIVPCVLISSMALL-
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79.4%;
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11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
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Best Local Similarity
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RESULT

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123
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                  79
                                                                                         140 ATNVVVRNUGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDEA
4 MLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVD
             QTINVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEA
                                                                                                                    GGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVL
                                        EKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTY
                                                                                                                                                                                                                                                                                                         Human, neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
brain tissue; screening; NAChR; antibody.
                                                                                                                                                                     ISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLG
                                                                                                                                                                                                                                                                                       Human neuronal nicotinic acetylcholine receptor alpha-7
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/label= TMD1
/note= "transmembrane domain"
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/label= TMD4
/note= "transmembrane domain"
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/note= "transmembrane domain"
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/label= TMD2
/note= "transmembrane domain"
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/label= signal
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N-PSDB; AAV12197.
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neurotransmitter;

Neuronal nicotinic acetylcholine receptor; nAChR;

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The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agoniets or antagoniets provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with nonned side effects than drugs identified e.g. screening with cells that express a variety of subtypes
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Human neuronal nicotinic acetylcholine receptor subunits and DNA - also transformed cells useful for screening cpds. which modulate activity of the receptor.
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                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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48.6%; Pred. No. 1.4e-122;
ive 75; Mismatches 138;
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                                                                            Claim 7; Page 80-81; 99pp; English
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.69
Watches 250; Conservative
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Neuronal nicotinic acetylcholine receptor alpha-7 subunit.

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502

standard; protein;

AAW09025 AAW09025

RESULT

AAW09025 ID AAWC XX AC AAWC XX DT 09-P XX XX XX

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                                                                                                                                                                                                                                                                                                                                                       The alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAT48239). Host cells, esp. mammalian cells or amphibian occytes, expressing the recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 ASVEMSAVA------PPPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 502;
                                                                                                                                                                                                                                                                                   sleic acids encoding nicotinic acetyl:choline receptor sub-sereening to determine the effect of drugs on the receptor.
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48.6%; Pred. No. 1.4e-122;
iive 75; Mismatches 138;
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                                                                                                                           96WO-US009775
                                                                                                                                                        95US-00484722
                                                                                                                                                                                    (SIBI-) SIBIA NEUROSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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           ligand-gated receptor
                                                                                                                                                                                                                                           1997-065463/06.
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Matches 250; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 502 AA;
                                                                                                                           37-JUN-1996;
                                                                                                                                                        07-JUN-1995;
                                         Homo sapiens
                                                                                               27-DEC-1996
                                                                                                                                                                                                               Elliott KJ,
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO1013, PRO1029, PRO310, PRO1029, PRO310, PRO1029, PRO1029, PRO1029, PRO1029, PRO1029, PRO1030, PRO1030, PRO1030, PRO1031, PRO1131, PRO1132, PRO1184, PRO1187, PRO1130, PRO1030, PRO1039, PRO334, PRO1317, PRO1131, PRO1184, PRO1187, PRO1281, PRO219, PRO339, PRO834, PRO1317, PRO1110, PRO2094, PRO2145 OR PRO2198, PRO and regorifsts can be used to inhibit tumour cell growth. The PRO POLYPEPTIGES and nuclectides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds conditions or disorders to be treatwist, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treatd with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, heptic carcinomas, sarcomas, compounds and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58366 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences.

CAAC58367 to AAC58396 and AAB24057 to AAC5806 represent human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosupressive; immunostimulant; antiianglogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; peptibelial disorder; stromal disorder; bastoccelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides encoding PRO polypeptides, useful in the diagnosis and prevention of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney AL,
461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO2145 protein sequence SEQ ID NO:77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A,
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                                                                                                                                                                                           AAB24088 standard; protein; 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US005028.
99WO-US012252.
99US-0141037P.
99US-0143048P.
99US-0145698P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-572270/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; drug design; protein co-ordinate data; schizophrenia; Alzheimer's disease; nicotine addiction; Tourette's syndrome; therapy; nootropic; neuroprotective.
                                                                                                                                                                                                129
                                                                                                                                                                                                                           186
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                                                                                                                                                                                                                                                                                                                                                                                                                366
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                                                                                                                    99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108. .115
/note= "conserved ligand-binding region, residues Trp108
and Tyr115 are essential"
exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residues Trp171
                                                                                                                                                                                      108 G------RMACSPTHDEHLLHGGQPPEGDPDLAKILEBVRYIANRFRCQDESEAVCSEW
                                                                                                                    LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQ11DVDEKN
                                                                                                                                 10 LALAASLIHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDERN
                                                                                                                                                                        OLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                                                                                           VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                           LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                                                                                                                                                                                                                                                                   247 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                                                                                                                                                                                                                                                     SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                                                                                                                                                                                                           GPGC
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                                                                                            Gaps
                                                                                           51;
                                                                Length 502;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "conserved ligand-binding region, and Tyr173 are essential"
 polynucleotide and protein sequences given in the
                                                                DB 3;
                                                               47.7%; Score 1258.5; DB 3;
48.6%; Pred. No. 1.4e-122;
ive 75; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                        367 ELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotinic acetylcholine receptor alpha7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                         250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 ASVEMSAVA-
                                                                             Similarity
             present invention
                                        AA;
                                        Sequence 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                  Query Match
                                                                                Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAChR). The sequence includes regions that are conserved throughout the various nAChR alpha subunits and which are essential for ligand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins (AChBPs) and analogues of ligand-gated ion channels, their use for screening ligands of ligand-gated ion channels. The water-soluble ligand-binding proteins are capable of channels. The water-soluble ligand-binding proteins are capable of structure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and the structure of AChBP is provided that are capable of binding a ligand of a ligand-comprise at least the amino acids of the AChBP care cereptor, and comprise at least the amino acids of the AChBP capable of binding a ligand of a ligand-capable of binding a ligand of a ligand. AChBP and also comprising amino acids determining binding to the ligand. In the chimeric proteins, at least the sesential amino acids of at least to corresponding amino acids, and preferably entire stretches have been substituted. New drugs can be developed that estectively intervene in cheuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder is Tourette's syndrome, channel is the nAChR, and the related disorder is Tourette's syndrome, and channel is the nAChR, and the related disorder is Tourette's syndrome, and also addiction to nicotine or schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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187 ISGYIPNGEWDLVGIPGKRSERPYECCKEPYPDVTFTVTWRRRTLYYGLNLLIPCVLISA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QILITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 ÖVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFHTN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
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                                                                                                                                                                                                                                                                                                                                                                              Water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
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  essential"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 47.7%; Score 1258.5; DB 4; Local Similarity 48.6%; Pred. No. 1.4e-122; Les 250; Conservative 75; Mismatches 138;
Cys212, Cys213 and Tyr217 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 252-254; 260pp; English.
                                                                                                                                                                                                                                                    (TEWE-) STICHTING TECH WETENSCHAPPEN.
                                                                                                                                                                                  2000EP-00200443.
                                                                                                                                     09-FEB-2001; 2001WO-EP001457.
                                                                                                                                                                                                                                                                                                                                        WPI; 2001-497071/54.
                                                                                                                                                                                                                                                                                                Sixma TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 502 AA;
                                              WO200158951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           schizophrenia.
                                                                                                                                                                                  10-FEB-2000;
31-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Special cell culture medium for treating cells and for inducing mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention, resulting in preferential calcium ion conductance by the cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLITNIWLSLEWNDYNLRWNDSBYGGVKDLRITPNKLWKPDVLMYNSADBGFDGTYQTN 126
                                                                                                    407
                                                                                                                                                                                                     SIFRIDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present
SVVLTVVVLLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
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                               -----PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, alpha7 nicotinic acetylcholine gated ion channel, 5-hydroxytryptamine, 5-HT3; calcium ion conductance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%; Score 1258.5; DB 4;
48.6%; Pred. No. 1.4e-122;
live 75; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wild-type human alpha7 ligand gated ion channel
                                                                                                                                                                                                                                                                                                            KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                                                                                         KFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494
                                                                                                      ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNI
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Matches 250; Conservative
                                                                                                                                                           367 ASVEMSAVA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-061524/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC90380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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contacting recombinant cells with a test compound

receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR

polypeptide

cells or

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QVLTINIWLQMSWIDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFHIN 129
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ISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRRILYYGLNLLIPCVLISA
                                                                                                                 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                              SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                        SIFRIDFRRSFVRPSIMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                                                         G-----RMACSPIHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW
                        VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                  SVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL
                                                                                                                                                                                                                                   nicotinic acetylcholine receptor; nNAChR; receptor; 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to nNAChR.
                                    The invention relates to a method for identifying compounds that antagonists or agonists of human neuronal nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuronal nicotinic acetylcholine receptor alpha 7 subunit.
                                                                                                                                                                                                           ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL----
                                                                                                                                                                                                                                                                                                      KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
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92US-00938154.
93US-00028031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     & CO INC
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                                                                                                                                                                                                                                                                                                                                                                                    ABG70492 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ion flux; alpha
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30-NOV-1992;
08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                  8 LALLA-LLPVSEQGPHEKRILLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                              MALLGFTLPPDSGEKLTLGVTLLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
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                                                                                                                                                                      QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
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                                                                                                                                                                                                         127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                                                                                                                                                                          SIFRIDFRRSFVRPSIMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; neuronal; nicotinic acetylcholine receptor; NAChR; drug
immunochemistry; NAChR alpha7 subunit; receptor.
                                                                                                   Length 502;
                                                                                                                   Indels
                                                                                                47.7%; Score 1258.5; DB 5;
48.6%; Pred. No. 1.4e-122;
iive 75; Mismatches 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB82435 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuronal NAChR alpha7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                   Conservative
                                                                                                         Similarity
                                                                              Sequence 502 AA;
                                                                                                                 250;
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ADA10874 standard; protein; 502

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isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synchetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-----RMACSPTHDEHLIHGGOPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460
                                                                                                                                                      Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVVVTVIVLQYHHHDPDGGKMPKMTRVILLINWCAMFLRMKRPGEDKVRPACOHKORRCSL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIFRIDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDOHCDMKFGSWTYDGNOLDLVLKDEAGGD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRILYYFFNLIVPCVLISS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MALLGFTLPPDSGEKLTLGVTTLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVVLTVVVLNYHHRTADIHEMPOWIKSVFLOWLPWILRMSRPGKKITRKTIMMNTRMREL
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                                                                     Elliott KJ;
                                                                                                                                                                                                                                                              invention relates to a suitable host cell transfected with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138; Indels
                                                                     Siegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.7%; Score 1258.5; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.4e-122; 75; Mismatches 138;
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                                                                     Chavez-Noriega LE,
                                                                                                                                                                                                                             Example; Page 130-131; 143pp; English
01-NOV-2000; 2000US-00703951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250; Conservative
                                                                   Claeps BO,
                                  (MERI ) MERCK & CO INC
                                                                                                    WPI; 2002-698532/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 502 AA;
                                                                 Gillespie A,
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New mucleic acid encoding an alpha-6 or a beta-3 subunit of a human neuronal nicotinic acetylcholine receptor (nAChR), useful for identifying compounds that modulate human neuronal nAChR activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 MALLGFILPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human neuronal nicotinic acetylcholine receptor nAChR. NAChR's form ligandgated ion channels that mediate synaptic transmissions between nerve and muscle and between neurons upon interaction with the neurotransmitter acetylcholine. The nucleic acid molecule is useful for identifying compounds that modulate human neuronal nAChR. The present sequence represents the amino acid sequence of the human neuronal nicotinic acetylcholine receptor, nAChR, alpha 7 subunit #1. Note: the present sequence is the sequence encoded by the nAChR alpha 7 subunit DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
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                                                                                         Human neuronal nicotinic acetylcholine receptor alpha 7 subunit #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 47.7%; Score 1258.5; DB 7; Length 502; Local Similarity 48.6%; Pred. No. 1.4e-122; Les 250; Conservative 75; Mismatches 138; Indels 51;
                                                                                                                      lpha 7 subunit; human; neuronal nicotinic acetylcholine recep
igand-gated ion channel; synaptic transmission; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 67-72; 63pp; English
                                                                                                                                                                                                                                                                                   96US-00660451.
                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                              & CO INC.
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                                                                                                                                                       transgenic, receptor
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SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                                   G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW
                                                                                                                                                                  ASVEMSAVA-------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                                                                                                                                             SIFRIDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
                                                                                                                                                                                                                                                                                                                                                                             367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL
                                                                                                                                                                                                                                                                                                                                       KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                              Length 502;
                                                                                                                                                                                                                                                                                 Indels
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48.6%; Pred. No. 1.4e-122;
ive 75; Mismatches 138;
                                                                                                                                                                                                                                              DB 7;
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Best Local Similarity 48.6'
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                                                                                                                                                                                                          Sequence 502 AA;
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neuronal tissue; gene therapy; tal nerve injury; chronic constriction injury; CCI;

segmental nerve injury; c) nerve injury; sNI; Chung.

Human; spinal spared

pain;

WO2003016475-A2

27-FEB-2003.

Homo sapiens

Human Protein P36544, SEQ ID NO 3171.

(first entry)

29-JAN-2004

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PP 714-MUG-2002; 2002W0-US025765.

PR 14-MUG-2001; 2001US-0313347P.

PR 01-NOV-2001; 2001US-031347P.

PR NOV-2001; 2001US-031347P.

PR 01-NOV-2001; 2001US-0314P.

PR 01-NOV-2001US-0314P.

PR 01-NOV-2001US-
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7; 187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246 247 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306 QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126 127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186 LALLA-LI PVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN 51; Length 502; 47.7%; Score 1258.5; DB 7; Length 48.6%; Pred. No. 1.4e-122; iive 75; Mismatches 138; Indels Query Match Best Local Similarity 48.65 Matches 250; Conservative Sequence 502 AA; 10 67 70 d à 원 ð g Op ₹ ð ð

366 407 407 465 460 SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366 307 SVVVTVIVLQYHHHDPDGGKMPKWTRVILLINWCAWFLRWKRPGEDKVRPACQHKQRRCSL 367 ASVEMSAVA-----PPP---ASNGNLLYIGERGLDGVHCVPTPDSGVVC 408 SIFRIDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 408 G-----RMACSPIHDEHLIHGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 466 KFAAMVVDRFCLFVFTLFTIJATVAVLLSAPHII 499 461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494 367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL 307 g à 셤  $\delta$ g  $\delta$ 

Search completed: May 7, 2004, 11:35:49 Job time : 44.0968 secs

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Run on:

Title:

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RESULT 1
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Heliothis virescens
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

(bases 1 to 3029)
Schulte,T., Oellers,N. and Adamczewski,M.
Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Cell
than to other insect nicotinic acetylcholine receptor alpha
                AF143847 3029 bp mRNA linear INV 27-MAY-1999 Heliothis virescens putative nicotinic acetylcholine receptor alpha
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Schulte, T., Oellers, N. and Adamczewski, M. Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG, 51368, Germany
                                                                                                                                                                                                                                                                                                                                                                                            virescens"
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/organism="Heliothis v:
/mol type="mRNA"
/db_xref="taxon:7102"
95. .1600
/note="hvnachra7-2"
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                                              7-2 subunit mRNA, complete cds.
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| 61 AspvalAspGluLysAsnGlnLeuLeulleThrAsnIleTrpLeuSerLeuGluTrpAsn [111111111111111111111111111111111111 | Db 455 GGGACCTACCAGACGTGGTGAAAGCGGCGCGCAGTTGCTCTACGTGCCACCT 514  QY 141 Gly1lePheLysSerThrCysLysWetAspileAlaTrpPheProPheAspAspGlnHis 160  bb 515 GGCATATTCAAGACCACATGCAAGATGGACATGCGTGTTTCCCTTCGACGACCACC 574  QY 161 CysAspMetLysPheGlySerTrpThrTyrAspGlyAsnGlnLeuAspLeuValleuLys 180  Db 575 TGTGATATGAAGTTCGGTAGCTGGACATTAGCGGCAATCAGTTGGTCTGGTGCTAAAA 634  QY 181 AspGluAlaGlyGlyAspLeuSerAspPheIleThrAsnGlyGlTTrpTyrLeuIleGly 200  Db 635 GATGAGGCGGGGTTTTTTTAAAAAAAAAAAAAAAAAAAA | 221 ThrPheThrIleMetIleArgArgArgThrLeuTyrTyrPhePheAsnLeuIleValPro                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | QY 321 ThralaaspileHisGluMetProGlnTrpileLysSerValPheLeuGlnTrpLeuPro 340  1055 ACAGCTGATATACATGAAATGCCACGTGGATAAAATCCACATTACCACTTGCTGCTTGTTGCTTGTTGTTGTTGTTGTTGTTGTTGT                                                                                                                                      |
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CCTCACGAGAAGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCG
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                                              ValAlaAsnGluSerGluProLeuGluValArgPheGlyLeuThrLeuGl
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KLWKPDVLMYNSADEGFDGTYGTVVVNYNSGSCLYVPPGIFKSTCKMOI AMFPEDDQH
CDMKRESWTYDGNOLDLVLXCBAGGLISDFTINGEWYLIGMEGKKWTITYACCPEPY
DVTFTIMIRRRTLYYFFNLI PROVIL SSMALLGFTLPPDSGEKLTGGVTLUSTTFU
NLABTLEDGYGSDAI PLIGTYRYCI MRYNSSYNTLTVVVLLNYNHRTADI THEMPQMIKSY
PLOWLPWILLNSR PROKIT PRYTIMNYNWASSYNLTUTVVLLNYNHRTADI THEMPQMIKSY
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   CGTCCACGATGGAAGACGTGGGCGGGCGGGTTGGGTAGCCACCATCGCGAGCTGCACCTC
                                              IleLeuArgGluLeuGlnPheIleThrAlaArgMetLysLysAlaAspGluGluAlaGlu
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FPEDDQHCBMKFGSVLMYNTOGOIDLYINSEDGGBLSDFITNGFWYLLANGSKCKTUTYN
CCPEPYVDITFIJQIRRRTLYYFFNILVPCVILISSWALLGFTLPPDSGEKITLGVTIL
ISLIVFLNLVAETLPQVSRDIPLGFYPROINGHWASSVLLGTVVVLNYHHRTADIHEM
PWWIKSYFLQMLPWILMRGRPGFKTTYKTILLSNRKKELEJKERSSKSLLANVLDIEDD
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/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
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to the sequence deposited in GenBank Accession Number
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha?, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-Co-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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/protein_id="AaM13394.1"
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Ephydroidea, Drosophilidae, Drosophila.
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Grauso, M. and Sattelle, D.B.
Direct Submission
Submittes (15-NOV-2000) Human Anatomy and Genetics Unit, University of Oxford, South
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/organism="Drosophila
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Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eterygota;

Roptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Endoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Endoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Endoptera; Endopterygota; Diptera; Drosophila.

Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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/note="results in glycine to asparagine substitution;
compared to the sequence deposited in GenBank Accession
Number AB003626"
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/note="results in asparagine to serine substitution,
compared to the sequence deposited in GenBank Accession
Number AE003626 and in variant clone"
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/note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3b
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/organism="Drosophila melanogaster"
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/note="compared to variant clone"
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to variant clone"
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/note="compared to variant
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/protein_id="AAM13393.1"
/db_xref="GI:20152847"
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/db_xref="taxon:7227"
/chromosome="2"
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/dev_stage="embryo"
1. .2023
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Grauso, M. and Sattelle, D.B.
Direct Submission
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DMESS4209

Drosophila melanogaster mRNA for nicotinic acetylcholine receptor subunit Dalpha6 (nAcRalpha-30D gene).

AJ554209

AJ554209.1 GI:29466434

DACRAlpha-30D gene; nicotinic acetylcholine receptor subunit
                                                                                                                            LeuGlnTrpLeuProTrpIleLeuArgMetSerArgProGlyLysLysIleThrArglys 355
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Direct Submission

Birect Submission

Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WCIE 6BT, UNITED KINGDOM
                 TACTICAATIGCATCATGTICATGGTCGCTCGTCGGTGGTGCTGACAGTAGTGCTCCTC
                                                          TyrPheAsnCysIleMetPheMetValAlaSerSerValValLeuThrValValValLeu
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila m
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DFRHTISGSQTALGSSASFGRPTTVEEHHTALGCNHKDLHLILKELQFITARNRKADD
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Dalphae
                                                                              receptor subunit
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                                                              /codon_start=1
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspleuArglleThrProAsnLysLeuTrpLysProAspValLeuMetTyrAsnSerAla
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                                                                                                                                 16 ValSerGluGlnGlyProHisGluLysArgLeuLeuAsnAlaLeuLeuAlaAsnTyrAsn
                                                                                                                                                                                                                   ThrLeuGluArgProValAlaAsnGluSerGluProLeuGluValArgPheGlyLeuThr
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Direct Submission

Submitted (19-DEC-2003) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
This clone was sequenced as cornary, presence of a polyA tail and contiguity
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes;
For further information about this sequence, including its location
(http://fruitfly.berkeley.edu) or send email to
codna@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="PLYBASE: FB9T0032151"

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ELQFITARMKRADDEAELIGDWKFAAMVVDRFCLIVFTILITITITUTUTULLSGAPHIIVQ
                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster

Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 169)

2 (bases 1 to 169)

3 (base)

4 (bases 1 to 169)

5 (champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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Mismatches:
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235 769 255 829 275

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                                                                                                                                                                                                                       PPEDDQHCEMKEGSWTYDGNQLDLVINSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA
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PPWIKSVFLQMLPWILRMPGRKITRYTILLSNRWKELELKERSSKSLLANVLDIDD
DFRHTISGSQTALGSSASFGRPTTVEEHHTAGCNHKOLHLILKELQFITARWKRADD
EAELIGDWKFAAMVVDRFCLIVFTLFITIATVTVLLSAPHIIVQ"
                                                          /codon_start=1
/product="nicotinic acetylcholine receptor Dalpha6 subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="nAcRalpha-30D"
/note="results in isoleucine to methionine substitution;
compared to variant clone"
                                      receptor; alternatively spliced; contains exons 3a and
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                                                                                                                                                                                                                                                                                                                                                                     /gene="nAcRalpha-30D"
/note="results in asparagine to glycine substitution;
compared to variant clone"
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                     'note="ion channel; neurotransmitter transmembrane
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'replace="t"
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Conservative:
Mismatches:
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/note="compared to variant
/replace="a"
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'gene="nAcRalpha-30D"
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Best Local Similarity:
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AF321445.1 GI:20152844
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
11973307
                                                                                                     LeuLeuAlaAsnValLeuAspIleAspAspAspPheArgHisGlyProProProAsn 395
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                     ThrileMetMetAsnThrArgMetArgGluLeuGluLeuLysGluArgSerSerLysSer
                                                                                                                                                                                    396 SerThrAlaSerThrGlyAsnLeuGlyProGlyCysSerIlePheArgThrAspPheArg
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
(bases 1 to 2023)
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
/chronosome="2"
/map="3001"
/dev_stage="embryo"
1. 2023
/gene="mAcRalpha-30D"
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Grauso, M. and Sattelle, D.B.
Direct Submission
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/db_xref="G1:20152851"
/translation="MOSPLPAGLSLFVLLIFLATIKESCQGPHEKRLINHLLSTYNTL
ERPVANESEBLEVKFGLTLQQIIDVDEKNQILTTNAMINDERNQLLITNLWISLEWN
DYNLRMNETEYGGYFVGLRITPRILMKEPVLMYNNSADEGFDGTYHTNIVVKRSGSCLYV
PPGIFKSTCKMDITWEPFEDDQHCEMRESWYYDROUDLYNSEDGGOLSDFITNGEW
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Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Submit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RAM, Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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AspGluGluAlaGluLeuIleSerAspTrpLysPheAlaAlaMetValValAspArgPhe
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Grauso,M. and Sattelle,D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2068)
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/mol_type="mRNA"
/db_xref="taxon:7227"
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/map="30D1"
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|                                                                         |                                                                                                                                            | Number AE003626" /replace="a" 1359 /gene="nAcRalpha-30D" /note="compared to the sequence deposited in GenBank Accession Number AE003626" /replace="c" 1605 | A / / / / / / / / / / / / / / / / / / | 2.9e-200 Length: 2068 2176.50 Matches: 418 Conservative: 31 Conservative: 37 Indels: 35 3 Gaps: 4 6 (1-501) x AF321448 (1-2068) AlaProMetLeuAlaAlaLeuAlaLeuLeuAlaLeuLeuPro 15 | TCCCGCTGCCAGCGTGCTGTTTGTCCTGTTGATCTTTCTGGCGATAATTAAA 444  ValSerGluchidlyProHisGluiysArgLeuLeuAsnalaLeuLeuAlaAsnTyrasn 35  ValSerGluchidlyProHisGluiysArgLeuLeuAsnalaLeuLeuAlaAsnTyrasn 35  GAAGCTGTCAAGAAAGCGCTGCTGAACAACGCTGCTGTTCTCCACCTACAAT 504  ThrLeuGluargProValAlaAsnaluSerGluProLeuGluValArgPheGlyLeuThr 55  ACGCTGGAGCGACCCGTGGAATGAATCGGAGCCCTGGAGGTTAAGTTCCGACTGACG 564 | GTGGTTA uTrpasn         GTGGAAC g1leThr         |
| variation                                                               | valiation                                                                                                                                  | variation<br>variation                                                                                                                                     | variation ORIGIN Alignment Scores     | Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match: DB: US-09-303-232-6 (1-501                                                                   | Db 385 Ti<br>Qy 16 Vi<br>Db 445 Gi<br>Qy 36 Ti<br>Db 505 Ac                                                                                                                                                                                                                                                                                                                          | Oy 56 Le  Db 565 C  Oy 63 -  Db 625 A  Db 685 G |

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/ db xref="G1:20152853"

/ translation="MDSPLPASIDSLEVLLIFLAIIKESCQSPHEKRLINHLLSTYNTL
ERPVADESEPLEWEGHTLQQIIDVDEKNQILTTNAMLNLEWNDYNLEWNEFEYGGYK
DIRITPNKLMKPDVLMYNSADBGFDGTYHTMIVVKHNGSCLYVPPGIFKSTCKMDITW
PPPDDQHCEMKFGSWTVDGNQLDLVLNSEDGGDLSPFITUSPDGGEKUTIVY
CCPBPYVDITFFIISTRRTLYFFNLIVPCVLISSMALLGFTLEPDGGEKUTIGVTI
ISLITVFLAILVAESMFTTSDAVPLIGVTILLSLTVFLAILOMETLPQVSDAIPLIGVTEN
ISLINFWARSELEKESSSSSLAAVLDIDDDFFHTIGGSGTAGSSSPGTYFTRKT
ILLSNRWKELELKESSSSSLAAVLDIDDDFFHTIGGSGTAGGSSAFGREFTIKT
TAIGCNHKDLHLILKELQFITARARKADDEAELIGDWKFAANVUDRFCLIVFTIIT
                                                                                                                                                                                                                                         Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type V (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
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                                                                                                     ACGCTCTTCACGATTATTGCAACGGTTACGGTGCTGCTCTCCGCTCCGCACATAATCGTG 1902
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receptor; alternatively spliced; contains exons 3a, 8a and
8b; contains two repeats of the transmembrane TM2 region"
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilae; Drosophila.

Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Nove and Highly Conserved Target of Adenosine Deaminase Acting on

RNA-mediated A-to-I Pre-mRNA Editing

Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OXI
                                ||||||||
TTGATCGCCGATTGGAAGTTCGCGGCAATGGTTGTGGATAGATTTTGTTTAATTGTTTTC
                                                                                  ThrLeuPheThrIleIleAlaThrValAlaValLeuLeuSerAlaProHisIleIleVal
         LeuIleSerAspTrpLysPheAlaAlaMetValValAspArgPheCysLeuPheValPhe
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/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
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/dev_stage="embryo"
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Grauso, M. and Sattelle, D.B.
Direct Submission
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PUBMED
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                                                                                           etLeuAlaAlaLeuAlaLeuLeuAlaLeuLeuProValSerGluGln---Gly
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Conservative:
Mismatches:
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